

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:51 ; Search time 62.83 Seconds
(without alignments)
27.982 Million cell updates/sec

Title: US-09-273-217-1
Perfect score: 78
Sequence: 1 FAFADERDSQFPSP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.15:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.protist:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	141	6 009074	009074 sus scrofa
2	78	100.0	476	6 008635	008635 bos taurus
3	78	100.0	499	6 09MTX3	09MTX3 oryctolagus
4	74	94.9	123	6 09N0E4	09N0E4 sus scrofa
5	74	94.9	141	6 009075	009075 sus scrofa
6	74	94.9	499	6 028293	028293 canis fam1
7	67	85.9	277	6 009076	009076 oryctolagus
8	67	85.9	277	6 09TUK6	09TUK6 oryctolagus
9	67	85.9	279	6 009080	009080 oryctolagus
10	67	85.9	279	6 09TUK7	09TUK7 oryctolagus
11	67	85.9	286	6 002911	002911 oryctolagus
12	60	76.9	529	11 061923	061923 mus musculu
13	59	75.6	494	13 091830	091830 oncorhynch
14	57	73.1	260	6 009079	009079 oryctolagus
15	54	69.2	955	5 076805	076805 drosophila
16	51	65.4	575	11 09Q0U4	09Q0U4 rattus sp.
17	51	65.4	857	11 003717	003717 mus musculu
18	51	65.4	858	4 014193	014193 homo sapien
19	51	65.4	858	6 018868	018868 sus scrofa

20	51	65.4	858	6 09M219	09M219 oryctolagus
21	51	65.4	876	13 091593	091593 xenopus lae
22	50	64.1	489	13 091781	091781 xenopus lae
23	50	64.1	511	4 016322	016322 homo sapien
24	50	64.1	725	6 028649	028649 oryctolagus
25	49	62.8	482	5 009937	009937 caenorhabdi
26	49	62.8	483	13 091829	091829 oncorhynch
27	49	62.8	593	6 028248	028248 canis fam1
28	49	62.8	602	11 092186	092186 mus musculu
29	48	61.5	27	13 073608	073608 gallus gall
30	47	60.3	27	13 073609	073609 gallus gall
31	47	60.3	662	13 09YGX8	09YGX8 gallus gall
32	46	59.0	516	6 028656	028656 oryctolagus
33	45	57.7	532	11 070259	070259 mus musculu
34	45	57.7	597	6 09T807	09T807 bos taurus
35	44	56.4	488	5 025376	025376 loligo opal
36	44	56.4	905	5 026344	026344 aplysia sp.
37	43	55.1	515	5 016968	016968 aplysia cal
38	43	55.1	898	13 091592	091592 xenopus lae
39	42	53.8	460	5 009658	009658 caenorhabdi
40	42	53.8	512	5 026597	026597 schistosoma
41	41	52.6	136	6 009077	009077 sus scrofa
42	41	52.6	374	2 09S3X6	09S3X6 streptomyce
43	41	52.6	478	5 091784	091784 polychoris
44	40	51.3	41	4 09UD44	09UD44 homo sapien
45	40	51.3	260	6 09XSQ0	09XSQ0 oryctolagus

ALIGNMENTS

RESULT 1
ID 009074 PRELIMINARY: PRT: 141 AA.
AC 009074;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE LLC2) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92125505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT *Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rat kidney and LLC-PK1 cells.";
RL Am J Physiol. 262:151-157(1992).
CC -I- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
CC INTERPRO: IPR000636; -
CC INTERPRO: IPR001622; -
CC INTERPRO: IPR003091; -
CC PFAM: PF00520; ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1 6 SEGMENT S3.
FT TRANSMEM <1 41 SEGMENT S4.
FT TRANSMEM 23 41

FT TRANSMEM 58 77 SEGMENT S5.
 FT TRANSMEM 119 141 SEGMENT S6.
 FT NON_TER 141 141
 SO SEQUENCE 141 AA; 15342 MW; C20E9B3B1412340 CRC64;

Query Match 100.0%; Score 78; DB 6; Length 141;
 Best Local Similarity 100.0%; Pred. No. 6; 2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDOPSPISIP 15
 Db 78 FAEDERDOPSPISIP 92

RESULT 2

008635 PRELIMINARY; PRT: 476 AA.

AC 008635; 01-NOV-1996 (TREMBLREL. 01, Created)

DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)

DT 01-OCT-2000 (TREMBLREL. 15, Last annotation update)

DE POTASSIUM CHANNEL PROTEIN KVL.2 (BGK5) (FRAGMENT).

OS Bos taurus (Bovine); Chordata; Vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RP SEQUENCE FROM N.A.

RX MEDLINE=92267180; PubMed=1587348;

RA Reid P.F., Pongs O., Dolly J.O.;

RT "Cloning of a bovine voltage-gated K⁺ channel gene utilizing partial

amino acid sequence of a dendrotoxin-binding protein from brain

cortex.";

RT FEBS Lett. 302:31-34(1992).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM

ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH

WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL

GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND

IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT

EVERY THIRD POSITION.

CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL

ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR

COMPARTMENTS.

CC -1- SIMILARITY: BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.

DR EMBL; X66185; CAA46953.1; -

DR INTERPRO: IPR000636; -

DR INTERPRO: IPR001622; -

DR INTERPRO: IPR003091; -

DR INTERPRO: IPR003131; -

DR PIRAM: PF00520; Ion_trans; 1.

DR PRAM: PF02214; K_tetra; 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Glycoprotein; Multigene family; Phosphorylation.

FT TRANSMEM 164 182 SEGMENT S1 (BY SIMILARITY).

FT TRANSMEM 222 243 SEGMENT S2 (BY SIMILARITY).

FT TRANSMEM 255 275 SEGMENT S3 (BY SIMILARITY).

FT TRANSMEM 293 311 SEGMENT S4 (BY SIMILARITY).

FT TRANSMEM 328 347 SEGMENT S5 (BY SIMILARITY).

FT TRANSMEM 389 411 SEGMENT S6 (BY SIMILARITY).

FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)

FT CARBOHYD 38 38 POTENTIAL.

FT CARBOHYD 207 207 POTENTIAL.

FT NON_TER 476 476

SO SEQUENCE 476 AA; 54152 MW; D350456A611C057D CRC64;

Query Match 100.0%; Score 78; DB 6; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2; 3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDOPSPISIP 15
 Db 348 FAEDERDOPSPISIP 362

RESULT 3

09MYX3 PRELIMINARY; PRT: 499 AA.

AC 09MYX3; 01-OCT-2000 (TREMBLREL. 15, Created)

DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLREL. 15, Last annotation update)

DE POTASSIUM CHANNEL SUBUNIT KV 1.2.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RA Thorndike K.S., Walsh M.P., Cole W.C.;

RT "Rabbit portal vein Kv 1.2."

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF284420; AAF91476.1; -

SO SEQUENCE 499 AA; 56692 MW; 7A4BF4608FB36308 CRC64;

Query Match 100.0%; Score 78; DB 6; Length 499;
 Best Local Similarity 100.0%; Pred. No. 2; 4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDOPSPISIP 15
 Db 348 FAEDERDOPSPISIP 362

RESULT 4

09NOE4 PRELIMINARY; PRT: 123 AA.

AC 09NOE4; 01-OCT-2000 (TREMBLREL. 15, Created)

DT 01-OCT-2000 (TREMBLREL. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLREL. 15, Last annotation update)

DE VOLTAGE-DEPENDENT K CHANNEL (FRAGMENT).

GN KVL.2.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RA Onya S., Imazumi Y.;

RT "porcine voltage-dependent K channel (KVL.2)."

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB043552; BAB07847.1; -

FT NON_TER 123 123

SO SEQUENCE 123 AA; 13532 MW; 232096561FED3461 CRC64;

Query Match 94.9%; Score 74; DB 6; Length 123;
 Best Local Similarity 93.3%; Pred. No. 3e-06;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDOPSPISIP 15
 Db 25 FAEDERDOPSPISIP 39

```

RESULT 5
ID 009075 PRELIMINARY: PRT: 141 AA.
AC 009075:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE LLC1) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92125505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:151-157(1992).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
CC INTERPRO: IPR000636; -
CC DR INTERPRO: IPR001622; -
CC DR INTERPRO: IPR003091; -
CC PFAM: PF00520; Ion_trans. 1.
CC PRINTS: PR00169; KCHANNEL.
CC DR PRINTS: PR00169; KCHANNEL.
CC KM Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
CC FT NON_TER 1 1
CC FT TRANSMEM <1 6 SEGMENT S3.
CC FT TRANSMEM 23 41 SEGMENT S4.
CC FT TRANSMEM 58 77 SEGMENT S5.
CC FT TRANSMEM 119 141 SEGMENT S6.
CC FT NON_TER 141 141
CC SQ SEQUENCE 141 AA; 15340 MW; 771ADPCGAB5255A CRC64;

Query Match 94.9%; Score 74; DB 6; Length 141;
Best Local Similarity 93.3%; Pred. No. 3.4e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSQPSIP 15
DB 78 FAEDERDSQPSIP 92

```

```

RA Sanders K.M., Horowitz B.;
RT "Cloning and expression of a Kv1.2 class delayed rectifier K+ channel
RT from canine colonic smooth muscle.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9659-9663(1993).
DR EMBL: L19740; AAA03607.1; -
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -
DR INTERPRO: IPR003131; -
DR PFAM: PF00520; Ion_trans. 1.
DR PFAM: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
DR Ionic channel.
KW SEQUENCE 499 AA; 56606 MW; 394FDA7D04CABEC8 CRC64;

Query Match 94.9%; Score 74; DB 6; Length 499;
Best Local Similarity 93.3%; Pred. No. 1.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEDERDSQPSIP 15
DB 348 FAEDERDSQPSIP 362

RESULT 7
ID 009076 PRELIMINARY: PRT: 277 AA.
AC 009076:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE KC2) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=92125505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:151-157(1992).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, LIVER, KIDNEY.
CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
CC INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
CC DR INTERPRO: IPR003131; -
CC PFAM: PF00520; Ion_trans. 1.
CC PFAM: PF02214; K_tetra. 1.
CC PRINTS: PR00169; KCHANNEL.
CC KM Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
CC FT NON_TER 1 1
CC FT TRANSMEM 83 101 SEGMENT S1.
CC FT TRANSMEM 141 162 SEGMENT S2.
CC FT TRANSMEM 174 193 SEGMENT S3.
CC FT TRANSMEM 206 224 SEGMENT S4.
CC FT TRANSMEM 241 260 SEGMENT S5.

```

SO	NON_TER	277	277	31819	MM;	A991F1FBFA72C649	CRC64;
SEQUENCE							
Query Match							
Best Local Similarity		85.9%;	Score 67;	DB 6;	Length 277;		
Matches 13;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
OY	1	FAEADERDSQFPS	13				
DB	265	FAEADERDSQFPS	277				
RESULT 8							
ID	Q9TUK6	PRELIMINARY;	PRT;	277	AA.		
AC	Q9TUK6;						
DT	01-MAY-2000	(TREMBLrel. 13, Created)					
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)					
DT	01-JUN-2000	(TREMBLrel. 14, Last annotation update)					
DE	VOLTAGE-GATED POTASSIUM CHANNEL ISOFORM 3 (FRAGMENT).						
OS	Oryctolagus cuniculus (Rabbit).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.						
OX	NCBI_TaxID=9986;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN-BRED NEW ZEALAND WHITE; TISSUE=KIDNEY;						
RC	MEDLINE=92125505; PubMed=1733291;						
RA	Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,						
RA	Igarashi P.;						
RT	"Isolation of putative voltage-gated epithelial K-channel isoforms						
RT	from rabbit kidney and LLC-PK1 cells.";						
RL	Am. J. Physiol. 262:0-0(1992).						
DR	EMBL; M81352; AAD43821.1; -						
DR	INTERPRO: IPR000636; -						
DR	INTERPRO: IPR003091; -						
DR	PFAM; PF00520; Ion_trans; 1.						
DR	PRINTS; PR00169; KCHANNEL.						
KW	Ionic channel.						
FT	NON_TER	1					
FT	NON_TER	277					
SO	SEQUENCE	277	AA;	31825	MM;	15FA3249E6FB8384	CRC64;
Query Match							
Best Local Similarity		85.9%;	Score 67;	DB 6;	Length 277;		
Matches 13;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
OY	1	FAEADERDSQFPS	13				
DB	265	FAEADERDSQFPS	277				
RESULT 9							
ID	Q09080	PRELIMINARY;	PRT;	279	AA.		
AC	Q09080;						
DT	01-NOV-1996	(TREMBLrel. 01, Created)					
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)					
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)					
DE	POTASSIUM CHANNEL PROTEIN (CLONE KC19) (FRAGMENT).						
OS	Oryctolagus cuniculus (Rabbit).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.						
OX	NCBI_TaxID=9986;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=KIDNEY;						
RC	MEDLINE=92125505; PubMed=1733291;						
RA	Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,						
RA	Igarashi P.;						
RT	"Isolation of putative voltage-gated epithelial K-channel isoforms						

RT					from rabbit kidney and LLC-PK1 cells."
RL	Am. J. Physiol.	262:151-157(1992).			
CC	-I-	FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT			
CC		AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF			
CC		MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO			
CC		THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A			
CC		POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN			
CC		ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.			
CC	-I-	SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-I-	TISSUE SPECIFICITY: BRAIN, LIVER, KIDNEY.			
CC	-I-	MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND			
CC		IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC		EVERY THIRD POSITION.			
CC	-I-	SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL			
CC		SUBFAMILY 1.			
DR	INTERPRO:	IPR000636; -			
DR	INTERPRO:	IPR003091; -			
DR	INTERPRO:	IPR003131; -			
DR	PFAM:	PF00520; Ion_trans; 1.			
DR	PFAM:	PF02214; K_tetra; 1.			
DR	PRINTS:	PP00169; KCHANNEL.			
KW		Ionic channel; transmembrane; Ion transport; Voltage-gated channel;			
KW		Glycoprotein; Multigene family.			
FT	NON TER	1			
FT	TRANSMEM	83	101		SEGMENT S1.
FT	TRANSMEM	141	162		SEGMENT S2.
FT	TRANSMEM	174	194		SEGMENT S3.
FT	TRANSMEM	211	229		SEGMENT S4.
FT	TRANSMEM	247	266		SEGMENT S5.
FT	CARBOHYD	126	126		POTENTIAL.
FT	NON TER	279	279		
SEQ	SEQUENCE	279 AA;	32034 MW;	E1E04D01746E896C	CRC64;

Query Match	Similarity	85.9%	Score	67	DB	6	Length	279	
Best Local	Similarity	100.0%	Pred. No.	0.00014					
Matches	13	Conservative	0	Mismatches	0	Indels	0	Gaps	0
OY	1	FAEADERDSQFPS	13						
DB	267	FAEADERDSQFPS	279						
RESULT	10								
ID	O9TUK7	PRELIMINARY;	PRT;	279	AA.				
AC	O9TUK7								
DT	01-MAY-2000	(TREMBLrel. 13, Created)							
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)							
DE	01-JUN-2000	(TREMBLrel. 14, Last annotation update)							
OS	VOLTAGG-GATED POTASSIUM CHANNEL ISOFORM 2 (FRAGMENT)								
OC	Oryctolagus cuniculus (Rabbit)								
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
CC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.								
OX	NCBI_TaxID=9986;								
RN	(1)								
RP	SEQUENCE FROM N.A.								
RC	STRAIN-BRED NEW ZEALAND WHITE; TISSUE-KIDNEY;								
RX	MEDLINE=92125505; PubMed=1733291;								
RA	Desir G V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,								
RT	Igarashi P.;								
RT	"Isolation of putative voltage-gated epithelial K-channel isoforms								
RT	from rabbit kidney and LLC-PK1 cells."								
RL	Am. J. Physiol. 262:0-0(1992).								
DR	EMBL: M81351; AAD43820.1; -.								
DR	INTERPRO: IPR000636; -.								
DR	INTERPRO: IPR003091; -.								
DR	PFAM: PF00520; Ion_Trans; 1.								
DR	PRINTS: PR00169; KCHANNEL.								
KW	Ionic channel.								
FT	NON_TER	1							
FT	NON_TER	1							
FT	NON_TER	279							
FT	NON_TER	279							
SEQUENCE	279	AA;	32022	MW;	E942DCB864906982	CRC64;			


```

Query Match      85.9%; Score 67; DB 6; Length 279;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FAERDERDSOFPs 13
        |||
Db      267 FAERDERDSOFPs 279

RESULT 11
ID 002911 PRELIMINARY; PRT; 286 AA.
AC 002911;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE KC6) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=KIDNEY;
RX MEDLINE=93158774; PubMed=7679255;
RA Desir G.V., Velazquez H.;
RT "Identification of a novel K-channel gene (KC22) that is highly
RT expressed in distal tubule of rabbit kidney."
RL Am. J. Physiol. 264:128-133(1993).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN AND TO A MUCH LESSER EXTENT, STOMACH,
CC SPLEEN, KIDNEY, AND HEART.
CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
DR EMBL: L01789; AAA31380.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1
FT TRANSMEM 86 106 SEGMENT S1.
FT TRANSMEM 148 168 SEGMENT S2.
FT TRANSMEM 180 203 SEGMENT S3.
FT TRANSMEM 215 239 SEGMENT S4.
FT TRANSMEM 252 275 SEGMENT S5.
FT CARBOHYD 129 129 POTENTIAL.
FT NON_TER 286
SQ SEQUENCE 286 AA; 32446 MW; BED94DAD21E12A07 CRC64;

Query Match      85.9%; Score 67; DB 6; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FAERDERDSOFPs 13
        |||
Db      274 FAERDERDSOFPs 286

```

```

RESULT 12
ID 061923 PRELIMINARY; PRT; 529 AA.
AC 061923;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE MORINE POTASSIUM CHANNEL PROTEIN.
GN MKI.6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Migeon M.B., Street V.A., Demas V.P., Tempel B.L.;
RL Epilepsy Res. 0:0-0(0).
DR EMBL: M6688; AAA39772.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 529 AA; 58673 MW; 336D78C069ABEADD CRC64;

Query Match      76.9%; Score 60; DB 11; Length 529;
Best Local Similarity 80.0%; Pred. No. 0.0057;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FAERDERDSOFPs 15
        |||
Db      396 FAERDDVSLFPsIP 410

RESULT 13
ID 091830 PRELIMINARY; PRT; 494 AA.
AC 091830;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE SHAKER-RELATED POTASSIUM CHANNEL TSHAI.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98146169; PubMed=9486764;
RA Nguyen T.D., Jeserich G.;
RT "Molecular structure and expression of shaker type potassium channels
RT in gill cells of trout CNS."
RL J. Neurosci. Res. 51:284-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Nguyen T.D., Jeserich G.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252301; AAF70087.1; -.
KW Ionic channel.
SQ SEQUENCE 494 AA; 55899 MW; AF66998F97F22CD4 CRC64;

Query Match      75.6%; Score 59; DB 13; Length 494;
Best Local Similarity 80.0%; Pred. No. 0.0082;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

OY 1 FAADERDSQFSP 15
 DB 343 FAADERDSQFSP 357

RESULT 14
 ID 009079 PRELIMINARY: PRT: 260 AA.

AC 009079: 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL PROTEIN (CLONE KC10) (FRAGMENT).
 OS ORCTOLAGUS CULICULUS (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=92125505; PubMed=1733291;
 RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
 RA Tigarashi P.;
 RT "Isolation of putative voltage-gated epithelial K-channel isoforms
 from rabbit kidney and LLC-PK1 cells.";
 RL Am. J. Physiol. 262:151-157(1992).

CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
 AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
 MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
 THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
 POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
 ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.

CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
 SUBFAMILY 1.

DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR003091; -;
 DR INTERPRO: IPR003131; -;
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family.

FT NON_TER 1 1
 FT TRANSMEM 85 103 SEGMENT S1.
 FT TRANSMEM 123 145 SEGMENT S2.
 FT TRANSMEM 156 176 SEGMENT S3.
 FT TRANSMEM 193 211 SEGMENT S4.
 FT TRANSMEM 228 247 SEGMENT S5.
 FT CARBOHYD 109 109 POTENTIAL.
 FT CARBOHYD 157 157 POTENTIAL.
 FT NON_TER 260 260
 SQ SEQUENCE 260 AA; 29833 MW; 82992930A9B7BFF CRC64;

Query Match 73.1%; Score 57; DB 6; Length 260;
 Best Local Similarity 84.6%; Pred. NO. 0.0097;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 FAADERDSQFSP 13
 DB 248 FAADERDSQFSP 260

RESULT 15
 ID 076805 PRELIMINARY: PRT: 955 AA.
 AC 076805:
 DT 01-NOV-1998 (Tremblrel. 08, Created)

DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE DELAYED RECTIFIER POTASSIUM CHANNEL.
 GN SHAB.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON S;
 RA Hegde P., Gu G.G., Chen D., Free S.J., Singh S.;
 RT "Mutational analysis of the Shab gene in Drosophila.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF084525; AAC33365.1; -
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR001622; -;
 DR INTERPRO: IPR003091; -;
 DR INTERPRO: IPR003131; -;
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 955 AA; 103132 MW; B245150FC90400CF CRC64;

Query Match 69.2%; Score 54; DB 5; Length 955;
 Best Local Similarity 66.7%; Pred. NO. 0.14;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 1 FAADERDSQFSP 15
 DB 597 FAEKENDTKFVSP 611

Search completed: February 2, 2001, 10:39:07
 Job time: 196 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:36 ; Search time 20.39 Seconds

(without alignments)
23.757 Million cell updates/sec

Title: US-09-273-217-1

Sequence: 1 FAEADERDSQFPSP 15

Scoring table: BIOSUM62

Gap0 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	499	1	CIR2_MOUSE
2	78	100.0	499	1	CIR2_XENLA
3	74	94.9	499	1	CIR2_HUMAN
4	61	78.2	529	1	CIR6_HUMAN
5	60	76.9	530	1	CIR6_RAT
6	56	71.8	273	1	CIR2_RABYT
7	54	69.2	924	1	CIRB_DROME
8	51	65.4	495	1	CIR1_HUMAN
9	51	65.4	495	1	CIR1_MOUSE
10	51	65.4	495	1	CIR1_RAT
11	51	65.4	853	1	CIR1_RAT
12	51	65.4	854	1	CIR1_HUMAN
13	49	62.8	601	1	CIR5_MOUSE
14	48	61.5	602	1	CIR5_MOUSE
15	48	61.5	602	1	CIR5_RAT
16	48	61.5	653	1	CIR4_HUMAN
17	48	61.5	654	1	CIR4_MOUSE
18	48	61.5	654	1	CIR4_MOUSE
19	48	61.5	655	1	CIR4_RAT
20	48	61.5	660	1	CIR4_BOVIN
21	46	59.0	523	1	CIR3_HUMAN
22	46	59.0	525	1	CIR3_RAT
23	46	59.0	528	1	CIR3_MOUSE
24	46	59.0	598	1	CIR5_RABIT
25	46	59.0	613	1	CIR5_HUMAN
26	43	55.1	297	1	YUBO_CAEEL
27	43	55.1	802	1	CIRB_RAT
28	43	55.1	806	1	CIRB_HUMAN
29	42	53.8	495	1	MURC_RICPR
30	41	52.6	769	1	SW16_KLUJA
31	40	51.3	616	1	CIR1_DROME
32	40	51.3	643	1	CIR4_DROME
33	40	51.3	656	1	CIR4_DROME

ALIGNMENTS

34	39	50.0	190	1	TREGU_SCHMA
35	39	50.0	266	1	ITLB_CEREL
36	39	50.0	556	1	YOT6_CAEEL
37	38	48.7	167	1	YXS5_CAEEL
38	38	48.7	293	1	BLAC_RHOCA
39	38	48.7	559	1	PAGT_HUOMA
40	38	48.7	559	1	PAGT_RAT
41	38	48.7	544	1	NUPI_YEAST
42	37	47.4	327	1	YGB7_ALCEO
43	37	47.4	399	1	MYC_CARAU
44	37	47.4	806	1	CIRB_CANFA
45	37	47.4	830	1	YDNI_SCHPO

RESULT 1
CIR2_MOUSE
ID CIR2_MOUSE STANDARD: PRT: 499 AA.
AC P15386; Q02010;
DT 01-APR-1990 (Rel. 14, Created)
DR 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (RCK5) (NGK1) (MK2) (HUKTV).
GN KCNA2.
OS Mus musculus (Mouse), and Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE-89255260; PubMed-2722779;
RA McKinnon D.;
RT "Isolation of a cDNA clone coding for a putative second potassium channel indicates the existence of a gene family."
RL J. Biol. Chem. 264:8230-8236(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT; TISSUE-BRAIN;
RX MEDLINE-90059914; PubMed-2555158;
RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B., Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
RT "Molecular basis of functional diversity of voltage-gated potassium channels in mammalian brain."
RL EMBO J. 8:3235-3244(1989).
RN [3]
RP REVISIONS.
RA Ludwig J.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE-91352097; PubMed-1715584;
RA Paulmichl M., Nasimith P., Herlitz R., Reed K., Boyle W.A., Nerbonne J.M., Peralta E.G., Clapham D.E.;
RT "Cloning and expression of a rat cardiac delayed rectifier potassium channel."
RL Proc. Natl. Acad. Sci. U.S.A. 88:7892-7895(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-MOUSE;
RX MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A., Ghoshani S., Tempel B.L., Gutman G.A.;
RT "A family of three mouse potassium channel genes with intronless coding regions."
RL Science 247:973-975(1990).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH

```
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J04731: AAA40819.1; -
DR EMBL: X16003: CAA34134.1; -
DR EMBL: M74449: AAA1867.1; -
DR EMBL: M30440: AAA39713.1; -
DR PIR: A33814: A33814.
DR PIR: S06709: S06709.
DR PIR: B40090: B40090.
DR HSSP: P03621: 21FN.
DR MGD: MGT:96659; KCNA2.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
DR KW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.
FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT CONFLICT 411 411 S -> F (IN REF. 4).
FT SEQUENCE 499 AA; 56700 MW; A8FEA6F3F594F42A CRC64;
SQ
Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FAEADERDSOPFSIP 15
Db 348 FAEADERDSOPFSIP 362
|||||
```

```
RESULT 2
CIR2_XENLA STANDARD; PRT; 499 AA.
ID CIR2_XENLA
AC P22739;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.2 (XSHA2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE-91026051; Pubmed-2223094;
RA Rabera A.B.;
RT "A potassium channel gene is expressed at neural induction.";
RL Neuron 5:691-701(1990)
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M35664: AAA49933.1; -
DR PIR: JH0313: JH0313.
DR HSSP: P03621: 21FN.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
DR KW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.
FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT SEQUENCE 499 AA; 56701 MW; 11445768038DCBB CRC64;
SQ
```

```
Query Match 100.0%; Score 78; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FAEADERDSOPFSIP 15
Db 348 FAEADERDSOPFSIP 362
|||||
```

```
RESULT 3
CIR2_HUMAN STANDARD; PRT; 499 AA.
ID CIR2_HUMAN
AC P16389;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.2 (RBK2) (HBK5) (NGK1)
DE (MK2) (HUKIV).
GN KCNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```

CC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CN      [1]
RN      RC
RP      SEQUENCE FROM N.A.
RC      TISSUE=BRAIN;
RA      Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RT      Mathew M.K.;
RT      "Human potassium channel genes: molecular cloning and functional
RL      expression.";
RL      Mol. Cell. Neurosci. 1:214-223(1990).
CC      -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC      ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC      CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC      MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC      WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC      GRADIENT.
CC      -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC      RATE OF INACTIVATION OF THE CHANNEL, WHILE THE TAIL MAY PLAY A ROLE
CC      IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC      TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC      -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC      CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC      EVERY THIRD POSITION.
CC      -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC      CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb.ch/announce/).
CC      or send an email to license@isb.ch).
CC      -----
DR      EMBL: L02752; AAA36141.1; -.
DR      HSSP: P03621; 21FN.
DR      MIM: 176262; -.
DR      INTERPRO: IPR000636; -.
DR      INTERPRO: IPR003091; -.
DR      PFMAM: PF00520; Ion_trans; 1.
DR      PRINTS: PR00169; KCHANNEL.
KW      Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW      Glycoprotein; Multigene family; Phosphorylation.
FT      TRANSMEM 164 182 SEGMENT S1.
FT      TRANSMEM 222 243 SEGMENT S2.
FT      TRANSMEM 255 275 SEGMENT S3.
FT      TRANSMEM 293 311 SEGMENT S4.
FT      TRANSMEM 328 347 SEGMENT S5.
FT      TRANSMEM 389 411 SEGMENT S6.
FT      CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT      SEQUENCE 499 AA: 56716 MW: 480371B4DA826C39 CRC64:
OY      Query Match 94.9%; Score 74; DB 1; Length 499;
OY      Best Local Similarity 93.3%; Pred. No. 9.8e-06;
OY      Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB      348 FAEADERDSQPSIP 362
RESULT 4
ID      C1K6_HUMAN STANDARD; PRT; 529 AA.
AC      P17658;
DT      01-AUG-1990 (Rel. 15, Created)
DT      01-AUG-1990 (Rel. 15, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)

```

```

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL6 (HK2).
GN KNA6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN.
RA MEDLINE=90269208; Pubmed-2347305;
RX Grube A., Schroeder K.H., Ruppersberg J.P., Stocker M., Drewes T.,
RT Beckh S., Pongs O.;
RT "Cloning and expression of a human voltage-gated potassium channel. A
RT novel member of the RCK potassium channel family.";
RL EMBO J. 9:11749-11756(1990).
CC CC
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONAL STATES IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBER, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC CC
CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X17622; CAA35623.1; -.
CC DR PIR; S15057; S15057.
CC DR MIM; 176257; -.
CC DR INTERPRO: IPR000636; -.
CC DR INTERPRO: IPR0003091; -.
CC DR PRFM; PF00520; Ion_Ctrans; 1.
CC DR PRINTS; PR00169; KCCHANNEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
CC FT TRANSMEM 175 193 SEGMENT S1.
CC FT TRANSMEM 263 284 SEGMENT S2.
CC FT TRANSMEM 296 316 SEGMENT S3.
CC FT TRANSMEM 340 360 SEGMENT S4.
CC FT TRANSMEM 376 396 SEGMENT S5.
CC FT TRANSMEM 437 457 SEGMENT S6.
CC FT MOD_RES 511 511 PHOSPHORYLATION (BY CAPK)
CC PT (PROBABLE)
CC SQ SEQUENCE 529 AA; 58728 MW; CFE0710A1FCDCD69F CRC64;
OY Query Match 78.2%; Score 61; DB 1; Length 529;
OY Best Local Similarity 80.0%; Pred No. 0.0022;
OY Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 FAEADDERDSQPSIP 15
OY |||||:|||||
DB 396 FAEADDSDLSFPSIP 410
RESULT 5
CIK6_RAT ID CIK6_RAT STANDARD; PRT; 530 AA.
AC P176559; P19025;
NC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

```

DT 15-JUL-1998 (Rel. 36, last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.6 (RCK2) (KV2).
GN KCNA6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN CORTEX;
RX MEDLINE=90269208; PubMed=2347305;
RA Gruppe A., Schroeter K.H., Ruppberg J.P., Stocker M., Drewes T.,
RA Beckh S., Pongs O.;
RT "Cloning and expression of a human voltage-gated potassium channel. A
RT novel member of the RCK potassium channel family.";
RL EMBO J. 9:1749-1756(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=90297965; PubMed=2361015;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Cloning and expression of cDNA and genomic clones encoding three
RT delayed rectifier potassium channels in rat brain.";
RL Neuron 4:929-939(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=91130598; PubMed=1993474;
RA Kirsch G.E., Drewe J.A., Verma S., Brown A.M., Joho R.H.;
RT "Electrophysiological characterization of a new member of the RCK
RT family of rat brain K⁺ channels.";
RL FEBS Lett. 278:55-60(1991).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright.. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X17621; CAA35622.1; -;
DR EMBL: M27159; AAA41499.1; ALT_SEQ.
DR PIR: JH0167;
DR PIR: S12786; S12786.
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR003091; -;
DR PFM: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 175 193 SEGMENT S1.
FT TRANSMEM 264 285 SEGMENT S2.
FT TRANSMEM 297 317 SEGMENT S3.
FT TRANSMEM 341 361 SEGMENT S4.
FT TRANSMEM 377 397 SEGMENT S5.

FT TRANSMEM 438 458 SEGMENT S6.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 222 222 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 512 512 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 528 528 (PROBABLE).
FT MOD_RES 528 528 PHOSPHORYLATION (BY CAPK)
FT CONFLICT 241 241 (POTENTIAL).
FT CONFLICT 333 333 S -> L (IN REF. 3).
FT CONFLICT 333 333 R -> G (IN REF. 2).
SQ SEQUENCE 530 AA; 58883 MW; 30A9774B66CF1DA5 CRC64;

Query Match 76.9%; Score 60; DB 1; Length 530;
Best Local Similarity 80.0%; Pred. No. 0.0033;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEDERSQFSPSP 15
DB 397 FAEDVDSDLESPSP 411

RESULT 6
CIRK2_RABIT STANDARD; PRT: 273 AA.
ID CIRK2_RABIT
AC 009081;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.2 (KC22) (FRAGMENT).
GN KCNA2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE=9212505; PubMed=1733291;
RA Desir G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K⁺-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:F151-F157(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROtetramer of potassium channel proteins (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, LIVER, KIDNEY.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
DR INTERPRO: IPR000636; -;
DR PFM: PF00520; Ion_trans; 1.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 84 102 SEGMENT S1.
FT TRANSMEM 137 158 SEGMENT S2.
FT TRANSMEM 190 190 SEGMENT S3.
FT TRANSMEM 206 224 SEGMENT S4.
FT TRANSMEM 241 260 SEGMENT S5.
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 273 273
SQ SEQUENCE 273 AA; 31722 MW; 86EA846FB2362F2C CRC64;

Query Match 71.8%; Score 56; DB 1; Length 273;
 Best Local Similarity 84.6%; Pred. No. 0.0083;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADERSOFS 13
 ||| ||| ||| ||| |||
 Db 261 FAEVDEPDSOFS 273

RESULT 7
 C1KB.DROME STANDARD; PRT: 924 AA.
 AC P17970;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAB (SHAB11).
 GN SHAB OR SHAB1.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90239553; PubMed-2333511;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "K+ current diversity is produced by an extended gene family
 conserved in Drosophila and mouse."
 RT Science 248:599-603(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90245668; PubMed-2336395;
 RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
 RT "Shal, Shab, and Shaw: three genes encoding potassium channels in
 Drosophila."
 RT Nucleic Acids Res. 18:2173-2174(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M32659; AAA28896.1; -
 DR PIR: S15058; S15058.
 DR HSSP: P01551; IACX.
 DR FLYBASE: FBgn0003383; Shab.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFAM: PF00520; Ion_trans.1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

Query Match 69.2%; Score 54; DB 1; Length 924;
 Best Local Similarity 66.7%; Pred. No. 0.073;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEADERSOFSIP 15
 ||| ||| ||| ||| |||
 Db 597 FAEKDEKTFVSIP 611

RESULT 8
 C1KL.HUMAN STANDARD; PRT: 495 AA.
 AC 009470;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1).
 GN KCNA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
 RA Mathew M.K.;
 RT "Human potassium channel genes: molecular cloning and functional
 expression."
 RT Mol. Cell. Neurosci. 1:214-223(1990).
 RN [2]
 RP VARIANTS AEK PHE-174; SER-239; ILE-249 AND ALA-408.
 RX MEDLINE-95144169; PubMed-7842011;
 RA Browne D.L., Gancher S.T., Nutt J.G., Brunt E.R.P., Smith E.A.,
 RA Kramer P., Litt M.;
 RT "Episodic ataxia/myokymia syndrome is associated with point mutations
 in the human potassium channel gene, KCNA1."
 RT Nat. Genet. 8:136-140(1994).
 RN [3]
 RP VARIANTS AEK ARG-177; ALA-226 AND ILE-404.
 RX MEDLINE-98260872; PubMed-9600245;
 RA Scheffer H., Brunt E.R.P., Mol G.J.J., van der Vlies P., Stulp R.P.,
 RA Verlind E., Mantel G., Aveyanov Y.N., Hofstra R.M.W., Buys C.H.C.M.;
 RT "Three novel KCNA1 mutations in episodic ataxia type I families."
 RT Hum. Genet. 102:464-466(1998).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE

KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 436 454 SEGMENT S1.
 FT TRANSMEM 474 495 SEGMENT S2.
 FT TRANSMEM 506 527 SEGMENT S3.
 FT TRANSMEM 536 561 SEGMENT S4.
 FT TRANSMEM 577 598 SEGMENT S5.
 FT TRANSMEM 638 659 SEGMENT S6.
 FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 756 756 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 885 885 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 888 888 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD.RES 690 690 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD.RES 731 731 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD.RES 796 796 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 SQ SEQUENCE 924 AA; 99698 MW; F4F74205C7020758 CRC64;

CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DISEASE: DEFECTS IN KCNA1 ARE THE CAUSE OF MYOKYMIA WITH PERIODIC
 CC ATAXIA (AEM) (PAROXYSMAL OR EPISODIC ATAXIA (EA)). A DISEASE
 CC CHARACTERIZED BY CONTINUOUS MUSCLE MOVEMENT (MYOKYMIA) AND
 CC PERIODIC ATAXIA.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L02750; AAA36139.1; -.
 DR HSSP: P03621; 21FN.
 DR MIM: 176260; -.
 DR MIM: 160120; -.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR003091; -.
 DR PFAM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation; Disease mutation.
 FT TRANSMEM 168 186 SEGMENT S1 (BY SIMILARITY).
 FT TRANSMEM 221 242 SEGMENT S2 (BY SIMILARITY).
 FT TRANSMEM 254 274 SEGMENT S3 (BY SIMILARITY).
 FT TRANSMEM 290 309 SEGMENT S4 (BY SIMILARITY).
 FT TRANSMEM 326 345 SEGMENT S5 (BY SIMILARITY).
 FT TRANSMEM 387 408 SEGMENT S6 (BY SIMILARITY).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
 FT (POTENTIAL).
 FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)
 FT (POTENTIAL).
 FT VARIANT 174 174 V -> F (IN AEKK).
 FT VARIANT 177 177 /FTId-VAR_001508.
 FT VARIANT 177 177 I -> R (IN AEKK).
 FT VARIANT 226 226 /FTId-VAR_001509.
 FT VARIANT 226 226 T -> A (IN AEKK).
 FT VARIANT 239 239 /FTId-VAR_001510.
 FT VARIANT 239 239 R -> S (IN AEKK).
 FT VARIANT 249 249 /FTId-VAR_001511.
 FT VARIANT 249 249 F -> I (IN AEKK).
 FT VARIANT 404 404 /FTId-VAR_001512.
 FT VARIANT 404 404 V -> I (IN AEKK).
 FT VARIANT 408 408 /FTId-VAR_001513.
 FT VARIANT 408 408 V -> A (IN AEKK).
 FT VARIANT 408 408 /FTId-VAR_001514.
 SQ SEQUENCE 495 AA; 56541 MW; 0A1BA1BD536F5CBA CRC64;

DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1 (MK1) (MBK1).
 GN KCNA1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP MEDLINE:90161966; PubMed:2305265;
 RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
 RA Ghanshani S., Tempel B.L., Gutman G.A.;
 RT "A family of three mouse potassium channel genes with intronless
 RT coding regions.";
 RL Science 247:973-975(1990).
 RN [2]
 RP MEDLINE:90161966; PubMed:2305265;
 RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
 RA Ghanshani S., Tempel B.L., Gutman G.A.;
 RT "Cloning of a probable potassium channel gene from mouse brain.";
 RL Nature 332:837-839(1988).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROOTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M30439; AAA39711.1; -.
 DR EMBL: Y00305; CA68408.1; -.
 DR PIR: S06378; S06378.
 DR PIR: A40090; A40090.
 DR HSSP: P03621; 21FN.
 DR MGD: MGI:96654; KCNA1.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR003091; -.
 DR PFAM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 168 186 SEGMENT S1.
 FT TRANSMEM 221 242 SEGMENT S2.
 FT TRANSMEM 254 274 SEGMENT S3.
 FT TRANSMEM 290 309 SEGMENT S4.
 FT TRANSMEM 326 345 SEGMENT S5.
 FT TRANSMEM 387 408 SEGMENT S6.
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
 FT (POTENTIAL).
 FT MOD_RES 446 446 PHOSPHORYLATION (BY CAPK)
 FT (POTENTIAL).
 SQ SEQUENCE 495 AA; 56409 MW; C9249F130E943D3D CRC64;

Query Match 65.48; Score 51; DB 1; Length 495;
 Best Local Similarity 66.78; Pred. No. 0.13;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEADERDPSIP 15
 ||||:|:|:|:|
 Db 346 FAEAEASHSSIP 360

RESULT 9
 CIKL_MOUSE STANDARD; PRT; 495 AA.
 ID CIKL_MOUSE
 AC P16388;
 DT 01-AUG-1990 (Rel. 15, Created)


```
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

DR EMBL: X16476; CAA34497.1; -

DR PIR: S05448; CHRTDL.

DR INTERPRO: IPR000636; -

DR INTERPRO: IPR003091; -

DR PFM: PF00520; Ion.trans; 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Glycoprotein; Multigene family; Phosphorylation.

FT DOMAIN 1 182

FT TRANSMEM 183 204 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 205 224 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 225 246 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 247 256 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 257 278 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 279 290 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 291 312 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 327 348 SEGMENT S4 (POTENTIAL).

FT DOMAIN 349 388 SEGMENT S5 (POTENTIAL).

FT TRANSMEM 389 410 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 411 853 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT MOD_RES 440 440 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD_RES 492 492 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT SEQUENCE 853 AA; 95280 MW; 7A0899839716165 CRC64;

SO

Query Match 65.4%; Score 51; DB 1; Length 853;

Best Local Similarity 66.7%; Pred. No. 0.23;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAADERDQFPSP 15

Db 347 FAEKEDDTKFKSP 361

RESULT 12

CIRK_HUMAN STANDARD; PRT; 854 AA.

ID CIRK_HUMAN

AC 014721;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DKK1).

GN KCNB1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]

RA SEQUENCE FROM N.A.

RA Ikeda S.R., Soler F., Zuhke R.D., Joho R.H., Lewis D.L.;

RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM

CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH

CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL

CC GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS

CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT

CC EVERY THIRD POSITION.

CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL

CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR

CC COMPARTMENTS.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER

CC CLASS: BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: L02840; AAA36156.1; -

DR MIM: 600397; -

DR INTERPRO: IPR000636; -

DR INTERPRO: IPR003091; -

DR PFM: PF00520; Ion.trans; 1.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Glycoprotein; Multigene family; Phosphorylation.

FT DOMAIN 1 182

FT TRANSMEM 183 204 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 205 224 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 225 246 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 247 256 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 257 278 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 279 290 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 291 312 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 313 326 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 327 348 SEGMENT S4 (POTENTIAL).

FT DOMAIN 349 388 SEGMENT S5 (POTENTIAL).

FT TRANSMEM 389 410 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 411 854 CYTOPLASMIC (POTENTIAL).

FT MOD_RES 440 440 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD_RES 492 492 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT SEQUENCE 854 AA; 95521 MW; 360DB3E45731EDA CRC64;

SO

Query Match 65.4%; Score 51; DB 1; Length 854;

Best Local Similarity 66.7%; Pred. No. 0.23;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAADERDQFPSP 15

Db 347 FAEKEDDTKFKSP 361

RESULT 13

CIRK_MUSPF STANDARD; PRT; 601 AA.

ID CIRK_MUSPF

AC P79197;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5.

GN KCNA5.

OS Mus musculus (Ferret).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

RN [1]

RA SEQUENCE FROM N.A.

RA Tissue=HEART ATRIUM;

RA Schweigel T., Folander K., Swanson R.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM

CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH

CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL

CC GRADIENT (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS

CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION
 CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U45979; AAB41145.1; -
 CC INTERPRO: IPR000636; -
 CC DR PFAM: PF00520; Ion_trans. 1.
 CC DR PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC FT TRANSMEM 240 258 SEGMENT S1.
 CC FT TRANSMEM 314 334 SEGMENT S2.
 CC FT TRANSMEM 345 366 SEGMENT S3.
 CC FT TRANSMEM 386 407 SEGMENT S4.
 CC FT TRANSMEM 422 443 SEGMENT S5.
 CC FT TRANSMEM 483 504 SEGMENT S6.
 CC FT DOMAIN 370 375 POLY-GLY
 CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 601 AA; 65889 MW; 142DB9F8CB843FE0 CRC64;
 CC
 CC Query Match 62.8%; Score 49; DB 1; Length 601;
 CC Best Local Similarity 60.0%; Pred. No. 0.35;
 CC Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 CC
 CC QY 1 FAEADERSOFSIP 15
 CC Db 442 FAEADNGETHFSIP 456
 CC
 CC RESULT 14
 CC CIK5_MOUSE STANDARD: PRT; 602 AA.
 CC AC Q61762;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 30-MAY-2000 (Rel. 39, Last annotation update)
 CC DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5 (KVL1-5).
 CC GN KCNA5.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-SWISS: TISSUP-HEART;
 CC RX MEDLINE:94043264; PubMed:8226976;
 CC RA Altai B., Lesage F., Ziliotti P., Guilleme E., Honore E.,
 CC RA Walman R., Hugnot J.-P., Mattei M.-G., Lazdunski M., Barhanin J.;
 CC RT "Multiple mRNA isoforms encoding the mouse cardiac Kvl1.5 delayed
 CC RT rectifier K+ channel."
 CC RL J. Biol. Chem. 268:24283-24289(1993).
 CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.

CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; KVL1-5 (SHOWN HERE), KVL1-5/5/
 CC AND KVL1-5/3'; ARE PRODUCED BY ALTERNATIVE SPLICING. KVL1-5/3' IS
 CC NON-FUNCTIONAL BUT INHIBITS EXPRESSION OF KVL1-5.
 CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND MODERATELY
 CC IN BRAIN. LOW LEVELS IN THYMUS, SKELETAL MUSCLE AND SPLEEN. NOT
 CC EXPRESSED IN LIVER, LUNG OR KIDNEY.
 CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L22218; AAA39365.1; -
 CC HSSP: P03621; 2IFN.
 CC DR MGD: MGI:96662; KCNA5.
 CC DR INTERPRO: IPR000636; -
 CC DR INTERPRO: IPR003091; -
 CC DR PFAM: PF00520; Ion_trans. 1.
 CC DR PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation;
 CC Alternative splicing.
 CC FT TRANSMEM 242 260 SEGMENT S1.
 CC FT TRANSMEM 316 336 SEGMENT S2.
 CC FT TRANSMEM 347 368 SEGMENT S3.
 CC FT TRANSMEM 387 408 SEGMENT S4.
 CC FT TRANSMEM 423 444 SEGMENT S5.
 CC FT TRANSMEM 484 505 SEGMENT S6.
 CC FT DOMAIN 373 376 POLY-GLY
 CC FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 CC FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 CC FT VARSPPLIC 1 200 MISSING (IN ISOFORM KVL1-5/3').
 CC FT VARSPPLIC 515 602 MISSING (IN ISOFORM KVL1-5/3').
 CC SQ SEQUENCE 602 AA; 66644 MW; FC2092B062FAC97 CRC64;
 CC
 CC Query Match 61.5%; Score 48; DB 1; Length 602;
 CC Best Local Similarity 66.7%; Pred. No. 0.54;
 CC Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 FAEADERSOFSIP 15
 CC Db 443 FAEADNQSOLSSIP 457
 CC
 CC RESULT 15
 CC CIK5_RAT STANDARD: PRT; 602 AA.
 CC ID CIK5_RAT
 CC AC P19024;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
 CC DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (KV1) (RCK7).
GN KCVAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA MEDLINE-90297965; PubMed-2361015;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Cloning and expression of cDNA and genomic clones encoding three
RT delayed rectifier potassium channels in rat brain.";
RL Neuron 4:929-939(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M27158; AAA1498.1; -;
DR PIR; JH0166; JH0166.
DR HSSP; P03621; 21FN.
DR INTERPRO; IPR000636; -;
DR INTERPRO; IPR003091; -;
DR PFAM; PF00520; Ion.trans.1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 242 260 SEGMENT S1.
FT TRANSMEM 316 336 SEGMENT S2.
FT TRANSMEM 347 368 SEGMENT S3.
FT TRANSMEM 387 408 SEGMENT S4.
FT TRANSMEM 423 444 SEGMENT S5.
FT TRANSMEM 484 505 SEGMENT S6.
FT DOMAIN 373 376 POLY-GLY.
FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ SEQUENCE 602 AA; 66552 MW; 6A784535FF226ED7 CRC64;

Oy 1 FAEADERSQPSIP 15
||||| |
Db 443 FAEADNHSHPSSIP 457

Search completed: February 2, 2001, 10:41:47
Job time: 311 sec

Query Match 61.5%; Score 48; DB 1; Length 602;
Best Local Similarity 66.7%; Pred. No. 0.54;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:47 ; Search time 38.22 Seconds
(without alignments)
26.649 Million cell updates/sec

Title: US-09-273-217-1

Sequence: 1 FAEADERDSQFPSP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	57	2	S09046
2	78	100.0	476	2	S21144
3	78	100.0	499	2	JH0313
4	78	100.0	499	2	I84204
5	78	100.0	499	2	A33814
6	74	94.9	499	2	I77466
7	74	94.9	499	2	A48672
8	67	89.9	2	146855	potassium channel
9	61	78.2	529	2	S12787
10	60	76.9	57	2	S09043
11	60	76.9	530	2	JH0167
12	54	69.2	924	2	B41359
13	54	69.2	924	2	S12746
14	51	65.4	57	2	S09042
15	51	65.4	495	2	I57680
16	51	65.4	495	2	A40090
17	51	65.4	495	2	B39113
18	51	65.4	853	1	CHRTD1
19	51	65.4	857	2	I36529
20	51	65.4	858	2	S31761
21	50	64.1	489	2	I51532
22	49	62.8	49	2	S09049
23	49	62.8	482	2	T15829
24	48	61.5	514	2	C48507
25	48	61.5	602	2	A43507
26	48	61.5	602	2	JH0166
27	48	61.5	653	2	A39922
28	48	61.5	654	2	S11049
29	48	61.5	654	2	E39113

30	48	61.5	660	2	S24125	potassium channel
31	46	59.0	57	2	S09044	potassium channel
32	46	59.0	57	2	S09047	potassium channel
33	46	59.0	523	2	A38101	potassium channel
34	46	59.0	523	2	I52990	voltage-gated pota
35	46	59.0	525	2	A43531	potassium channel
36	46	59.0	528	2	I84205	potassium channel
37	46	59.0	598	2	S66659	potassium channel
38	46	59.0	613	2	A56031	potassium channel
39	45	57.7	57	2	S09048	potassium channel
40	45	57.7	57	2	S09045	potassium channel
41	45	57.7	597	2	S51212	BAK5 protein - bov
42	43	55.1	297	2	T21387	hypothetical prote
43	43	55.1	802	2	JH0595	potassium channel
44	42	53.8	460	2	T27759	hypothetical prote
45	42	53.8	495	2	C71679	UDP-n-acetylurama

ALIGNMENTS

RESULT 1
S09046
potassium channel protein MK-5 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence-revision 30-Sep-1991 #text-change 18-Jun-1993
C:Accession: S09046
R:Belsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, F.E.S. Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
A:Reference number: S09042; MUID:90235950
A:Accession: S09046
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match 100.0%; Score 78; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADERDSQFPSP 15
DB 11 FAEADERDSQFPSP 25
RESULT 2
S21144
potassium channel protein RCK5 - bovine (fragment)
N:Alternate names: potassium channel protein 2
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence-revision 05-Apr-1995 #text-change 05-Nov-1999
C:Accession: S21144; A23668; A33158
R:Reid, P.F.; Pongs, O.; Dolly, J.O.
A:Title: Cloning of a bovine voltage-gated K(+) channel gene utilising partial amino
A:Reference number: S21144; MUID:92267180
A:Accession: S21144
A:Molecule type: DNA
A:Residues: 1-476 <RET>
A:Cross-references: GR:X66185; NID:9395206; PIDN:CA446953.1; PID:9395207
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 320-
R:Scott, V.E.S.; Parcell, D.N.; Keen, J.N.; Findlay, J.B.C.; Dolly, J.O.
J. Biol. Chem. 269, 20094-20097, 1990
A:Title: alpha-bendroxiol in acceptor from bovine brain is a K(+) channel protein. Evid
A:Reference number: A23668; MUID:91056043
A:Accession: A23668
A:Molecule type: protein
A:Residues: 2-28 <SC0>
R:Newitt, R.A.; Houamed, K.M.; Rehm, H.; Tempel, B.L.
submitted to the Protein Sequence Database, February 1991
A:Reference number: A33158
A:Accession: A33158

A:Molecule type: protein
A:Residues: 2-27 <NEW>
C:Keywords: glycoprotein; transmembrane protein
F:38,207,466/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 78; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQPSIP 15
|||||
Db 348 FAEADERDSQPSIP 362

RESULT 3
JH0313
potassium channel protein Xsha2 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: JH0313

R:Ribera, A.B.
Neuron 5, 691-701, 1990
A:Title: A potassium channel gene is expressed at neural induction.
A:Reference number: JH0313; MUID:91026051

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-499 <RTB>

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQPSIP 15
|||||
Db 348 FAEADERDSQPSIP 362

RESULT 4
I84204
potassium channel protein MK2 - mouse

C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: B40090; I84204

R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanashan, S.; Tempel, B.L.
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regions.
A:Reference number: A40090; MUID:90161996

A:Accession: B40090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-499 <CHA>
A:Cross-references: GB:M30440; NID:q199706; PIDN:AAA3713.1; PID:q199707
C:Genetics:
A:Gene: MK2

Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQPSIP 15
|||||
Db 348 FAEADERDSQPSIP 362

RESULT 5
A33814
potassium channel KVL2 - rat
N:Alternate names: potassium channel RCK5; potassium channel RK2; RAK
C:Species: Rattus norvegicus (Norway rat)

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 05-Nov-1999
C:Accession: A33814; C39113; S06709; I59204
R:McKinnon, D.
J. Biol. Chem. 264, 8230-8236, 1989

A:Title: Isolation of a cDNA clone coding for a putative second potassium channel ind
A:Reference number: A33814; MUID:89255260
A:Accession: A33814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-499 <MCK>

A:Cross-references: GB:J04731; NID:q203154; PIDN:AAA40819.1; PID:q203155
R:Roberts, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chann
A:Reference number: A39113; MUID:91156694
A:Accession: C39113

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA

A:Residues: 1-12,24-499 <ROB>
R:Stuehmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Giese, E.
EMBO J. 8, 3235-3244, 1989

A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
A:Reference number: S06708; MUID:90059914
A:Accession: S06709

A:Molecule type: mRNA
A:Residues: 1-247, 'SC', 250-261, 'T', 263-282, 'HTNR', 288-291, 'T', 293-499 <STU>
A:Cross-references: EMBL:X16003

R:Paulmichl, M.; Nasmit, P.; Herlitz, R.; Reed, K.E.; Boyle, W.A.; Nerbonne, J.M.;
Proc. Natl. Acad. Sci. U.S.A. 88, 7892-7895, 1991
A:Title: Cloning and expression of a rat cardiac delayed rectifier potassium channel.

A:Reference number: I59204; MUID:91352097
A:Accession: I59204
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-410, 'F', 412-499 <RES>
A:Cross-references: GB:M74449; NID:q206548; PIDN:AAA19867.1; PID:q206549
A:Experimental source: heart atrium

C:Genetics:
A:Gene: RAK
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane

F:164-182/Domain: transmembrane #status predicted <TM1>
F:222-243/Domain: transmembrane #status predicted <TM2>
F:255-275/Domain: transmembrane #status predicted <TM3>
F:288-311/Domain: transmembrane #status predicted <TM4>

F:328-347/Domain: transmembrane #status predicted <TM5>
F:353-372/Domain: transmembrane #status predicted <TM6>
F:373-381/Domain: transmembrane beta strand #status predicted <TM7>
F:389-411/Domain: transmembrane #status predicted <TM8>
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:449/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre
Query Match 100.0%; Score 78; DB 2; Length 499;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAEADERDSQPSIP 15
|||||
Db 348 FAEADERDSQPSIP 362

RESULT 6
I77466
potassium channel - human

C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I77466

R:Ramashwami, M.; Gautam, M.; Kamh, A.A.; Rudy, B.; Tanoye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990
A:Title: Human potassium channel genes: molecular cloning and functional expression.

A:Reference number: I57680
A:Accession: I77466
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-499 <RES>
 A:Cross-references: GB:L02752; NID:9186668; PIDN:AAA36141.1; PID:9186669

Query Match
 Best Local Similarity 93.3%; Score 74; DB 2; Length 499;
 Pred. No. 1.8e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADERDSQFSPSIP 15
 |||||||:||||||
 Db 348 FAEADERESQFSPSIP 362

RESULT 7
 A48672
 delayed rectifier potassium channel Kv1.2, smooth muscle - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Nov-1999
 C:Accession: A48672
 R:Hart, P.J.; Overlurf, K.E.; Russell, S.N.; Carl, A.; Hume, J.R.; Sanders, K.M.; Horow
 Proc. Natl. Acad. Sci. U.S.A. 90, 9659-9663, 1993
 A:Title: Cloning and expression of a K-v1.2 class delayed rectifier K(+) channel from ca
 A:Reference number: A48672; MUID:94022435
 A:Accession: A48672
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-499 <HAR>
 A:Cross-references: GB:L19740; NID:9304651; PIDN:AAA03607.1; PID:9304652
 A:Keywords: smooth muscle

Query Match
 Best Local Similarity 93.3%; Score 74; DB 2; Length 499;
 Pred. No. 1.8e-05;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADERDSQFSPSIP 15
 |||||||:||||||
 Db 348 FAEADERESQFSPSIP 362

RESULT 8
 146855
 voltage-gated potassium channel - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
 C:Accession: 146855
 R:Desir, G.; Velazquez, H.
 Am. J. Physiol. 264, 128-133, 1993
 A:Title: Identification of a novel K-channel gene (KC22) that is highly expressed in dis
 A:Reference number: 146855
 A:Accession: 146855
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-286 <DES>
 A:Cross-references: GB:L01789; NID:9165448; PIDN:AAA1380.1; PID:9165449

Query Match
 Best Local Similarity 85.9%; Score 67; DB 2; Length 286;
 Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADERDSQFSPS 13
 |||||||:||||||
 Db 274 FAEADERDSQFSPS 286

RESULT 9
 S12787
 potassium channel KCNA2 - human
 N:Alternate names: potassium channel HBK2
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: S12787; S15057
 R:Grube, A.; Schroeter, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.;
 EMBO J. 9, 1749-1756, 1990
 A:Title: Cloning and expression of a human voltage-gated potassium channel. A novel m
 A:Reference number: S12786; MUID:90269208
 A:Accession: S12787

A:Molecule type: mRNA
 A:Residues: 1-529 <GRU>
 A:Cross-references: EMBL:X17622
 R:Pongs, O.
 submitted to the EMBL Data Library, November 1989

A:Reference number: S15057
 A:Accession: S15057

A:Molecule type: mRNA
 A:Residues: 1-57, 59-529 <PON>
 A:Cross-references: EMBL:X17622; NID:932032; PIDN:CAA35623.1; PID:932033
 C:Genetics:

A:Gene: GDB:KCNA2; HK4; KV1.2
 A:Cross-references: GDB:128062; OMIM:176262
 C:Keywords: glycoprotein; ion channel; transmembrane protein
 F:175-193/Domain: transmembrane #status predicted <TM1>
 F:263-284/Domain: transmembrane #status predicted <TM2>
 F:296-316/Domain: transmembrane #status predicted <TM3>
 F:340-359/Domain: transmembrane #status predicted <TM4>
 F:376-395/Domain: transmembrane #status predicted <TM5>
 F:437-458/Domain: transmembrane #status predicted <TM6>

Query Match
 Best Local Similarity 78.2%; Score 61; DB 2; Length 529;
 Pred. No. 0.0042;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEADERDSQFSPSIP 15
 |||||||:||||||
 Db 396 FAEADDDSLFSPSIP 410

RESULT 10
 S09043
 potassium channel protein MK-2 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: S09043
 R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
 FEBS Lett. 263, 121-126, 1990
 A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
 A:Reference number: S09042; MUID:90235950
 A:Accession: S09043
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-57 <BET>

Query Match
 Best Local Similarity 76.9%; Score 60; DB 2; Length 57;
 Pred. No. 0.00053;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEADERDSQFSPSIP 15
 |||||||:||||||
 Db 11 FAEADVDLSFSPSIP 25

RESULT 11
 JH0167
 potassium channel Kv1.6 - rat
 N:Alternate names: potassium channel Kv2; potassium channel RCK2
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Nov-1999
 C:Accession: JH0167; S12786
 R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Polander, K.;
 Neuron 4, 929-939, 1990
 A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec
 A:Reference number: JH0166; MUID:90297965

A:Accession: JH0167
A:Molecule type: mRNA
A:Residues: 1-530 <SWA>
A:Cross-references: GB:M27159
A:Experimental source: brain
R:Gruppe, A.; Schroeter, K.H.; Ruppersberg, J.P.; Stoecker, M.; Drewes, T.; Beckh, S.; Port
EMBO J. 9, 1749-1756, 1990
A:Title: Cloning and expression of a human voltage-gated potassium channel. A novel mem
A:Reference number: S12786; MUID:90269208
A:Accession: S12786
A:Molecule type: mRNA
A:Residues: 1-332, 'R', 334-530 <GRU>
A:Cross-references: EMBL:X17621; NID:957666; PIDN:CAA35622.1; PID:957667
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane bet
F:175-193/Domain: transmembrane #status predicted <TM1>
F:264-285/Domain: transmembrane #status predicted <TM2>
F:297-317/Domain: transmembrane #status predicted <TM3>
F:341-360/Domain: transmembrane #status predicted <TM4>
F:377-396/Domain: transmembrane #status predicted <TM5>
F:412-421/Domain: transmembrane beta strand #status predicted <TMB1>
F:422-430/Domain: transmembrane beta strand #status predicted <TMB2>
F:438-459/Domain: transmembrane #status predicted <TM6>
F:512/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predic
F:528/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic

Query Match 76.9%; Score 60; DB 2; Length 530;
Best Local Similarity 80.0%; Pred. No. 0.0063;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEDERDQFPSP 15
|||||: || |||||
Db 397 FAEDVDVSLPSP 411

RESULT 12
B41359
potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Feb-1997
C:Accession: B41359
R:Butler, A.; Wei, A.; Baker, K.; Salkoff, L.
Science 243, 943-947, 1989
A:Title: A family of putative potassium channel genes in Drosophila.
A:Reference number: A41359; MUID:89146139
A:Accession: B41359
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
A:Cross-references: GB:M32659
C:Genetics:
A:Gene: FlyBase:Shab
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drk1

Query Match 69.2%; Score 54; DB 2; Length 924;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEDERDQFPSP 15
|||||: || |||||
Db 597 FAEDKDKTKFVSP 611

RESULT 13
S12746
potassium channel protein shab11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999
C:Accession: S12746; S15058
R:Butler, A.; Wei, A.; Salkoff, L.
Nucleic Acids Res. 18, 2173-2174, 1990

A:Title: Shal, Shab, and Shaw: three genes encoding potassium channels in Drosophila.
A:Reference number: S12746; MUID:90245668
A:Accession: S12746
A:Molecule type: mRNA
A:Residues: 1-924 <BUT>
A:Cross-references: EMBL:M32659
R:Butler, A.; Wei, A.; Salkoff, L.
submitted to the EMBL Data Library, March 1990
A:Description: Shal, Shab, and Shaw: Three genes encoding potassium channels in Droso
A:Reference number: S15058
A:Accession: S15058
A:Molecule type: mRNA
A:Residues: 1-625, 'Y', 628-924 <BUT>
A:Cross-references: EMBL:M32659; NID:9158458; PIDN:AAA28896.1; PID:9158459
C:Genetics:
A:Gene: shab11
A:Cross-references: FlyBase:FBgn0003383
C:Superfamily: potassium channel protein drk1
C:Keywords: ion channel; potassium channel; transmembrane protein

Query Match 69.2%; Score 54; DB 2; Length 924;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAEDERDQFPSP 15
|||||: || |||||
Db 597 FAEDKDKTKFVSP 611

RESULT 14
S09042
potassium channel protein MK-1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09042
R:Bertholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
A:Reference number: S09042; MUID:90235950
A:Accession: S09042
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match 65.4%; Score 51; DB 2; Length 57;
Best Local Similarity 66.7%; Pred. No. 0.022;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEDERDQFPSP 15
|||||: || |||||
Db 11 FAEDAEASHFSSP 25

RESULT 15
I57680
potassium channel KCNA1 - human
N:Alternate names: potassium channel protein HKC-1
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
C:Accession: I57680; A60173
R:Ramashwami, M.; Gautam, M.; Kamp, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990
A:Title: Human potassium channel genes: molecular cloning and functional expression.
A:Reference number: I57680
A:Accession: I57680
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-495 <RAM>
A:Cross-references: GB:I02750; NID:g186662; PIDN:AAA36139.1; PID:g186663
R:Freeman, S.N.; Conley, E.C.; Brennand, J.C.; Russell, N.J.W.; Bremner, W.J.
Biochem. Soc. Trans. 18, 891a, 1990

A:Title: Cloning and characterization of a cDNA encoding a human brain potassium channel
A:Reference number: A60173; MUID:91192386
A:Accession: A60173
A:Molecule type: mRNA
A:Residues: 263-264,266-314,'R' <FRE>
C:Genetics:
A:Gene: GDB:KCNAL; RBK1; HUK1; MBK1; AEMK; KVL.1
A:Cross-references: GDB:127903; OMIM:176260
A:Map position: 12p13-12p13

Query Match 65.4%; Score 51; DB 2; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 FAADERDSQFPSIP 15
|||||:| | | | |
DB 346 FAFAEEAESHFSSIP 360

Search completed: February 2, 2001, 10:37:10
Job time: 83 sec

THIS PAGE IS BLANK

Db 349 FAEKDEDTFKSIP 363

RESULT 2

US-08-527-152-2

Sequence 2, Application US/08527152

Patent No. 5627065

GENERAL INFORMATION:

APPLICANT: Chandu, Kanianthara G.

APPLICANT: Cahalan, Michael D.

APPLICANT: Glissmer, Stephan

APPLICANT: Goldin, Alan L.

APPLICANT: Delniet, Brent A.

APPLICANT: Gutman, George A.

APPLICANT: Wasmuth, John J.

TITLE OF INVENTION: Assay, Methods and Products Based On n

TITLE OF INVENTION: K+ Channel Expression

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,

ADDRESSEE: Attn: W.H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/527,152

FILING DATE: UNKNOWN

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/170,418

FILING DATE: 20-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/558,568

FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-5444-2/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 528 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-527-152-2

Query Match

Best Local Similarity 59.0%; Score 46; DB 2; Length 528;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAEADERDQFPSTIP 15

Db 371 FAEADDPSSGFSNIP 385

RESULT 3

US-08-288-405A-10

Sequence 10, Application US/08288405A

Patent No. 5559009

GENERAL INFORMATION:

APPLICANT: Chandu, Kanianthara G.

APPLICANT: Kalman, Katalin

APPLICANT: Chandu, Gritscha

APPLICANT: Gutman, George A.

TITLE OF INVENTION: A No. 5559009el Voltage-gated Potassium Channel

TITLE OF INVENTION: Gene

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,

ADDRESSEE: Attn: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/288,405A

FILING DATE: 10-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/207,431

FILING DATE: 04-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-59844-1/WHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 532 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-288-405A-10

Query Match

Best Local Similarity 57.7%; Score 45; DB 1; Length 532;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAEADERDQFPSTIP 15

Db 408 FAEVDVDTHTFTSIP 422

RESULT 4

US-07-789-915A-2

Sequence 2, Application US/07789915A

Patent No. 5212058

GENERAL INFORMATION:

APPLICANT: Baker, Rohan T.

APPLICANT: Tobias, John W.

APPLICANT: Varshavsky, Alexander

TITLE OF INVENTION: Ubiquitin-Specific Proteases

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS


```

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,915A
; FILING DATE: 19911108
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-5091AA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1121 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-789-915A-2

Query Match          46.8%; Score 36.5; DB 1; Length 1121;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 FAEADERDSQFSPSIP 15
Db 601 YARVDE-DQPPFAPV 614

RESULT 5
US-08-005-002C-2
; Sequence 2, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/005,002C
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,915
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0528
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-005-002C-2
```

```

Query Match          46.8%; Score 36.5; DB 1; Length 1121;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 FAEADERDSQFSPSIP 15
Db 601 YARVDE-DQPPFAPV 614

RESULT 6
US-08-487-203A-2
; Sequence 2, Application US/08487203A
; Patent No. 5683904
; GENERAL INFORMATION:
; APPLICANT: Baker, Rohan T.
; APPLICANT: Tobias, John W.
; APPLICANT: Varshavsky, Alexander
; TITLE OF INVENTION: Ubiquitin-specific Proteases
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: U.S.A.
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,203A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/005,002
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: MIT-5091AAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0528
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1121 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-203A-2

Query Match          46.8%; Score 36.5; DB 1; Length 1121;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 FAEADERDSQFSPSIP 15
Db 601 YARVDE-DQPPFAPV 614

RESULT 7
5476657-1
; Patent No. 5476657
; APPLICANT: POTTER, ANDREW A.
; TITLE OF INVENTION: PASTURELLA HAEMOLYTICA LEUKOTOXIN
; COMPOSITIONS AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
```

```

: APPLICATION NUMBER: US/08/15,537
: FILING DATE: 09-FEB-1993
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 504,850
: FILING DATE: 05-APR-1990
: APPLICATION NUMBER: 335,018
: FILING DATE: 07-APR-1989
:
: SEQ ID NO:1
: LENGTH: 1334
: 5476657-1

```

Query Match	46.8%;	Score 36.5;	DB 5;	Length 1334;
Best Local Similarity	46.7%;	Pred. No. 2.2e+02;		
Matches	7;	Conservative	3;	Mismatches 4;
				Indels 1;
				Gaps 1

```

RESULT      8
US-07-908-253-3
; Sequence 3, Application US/07908253
; Patent No. 5534256
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: HARLAND, RICHARD J.
; TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
; TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBERTA L. ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,253
; FILING DATE: 19920702
; CLASSIFICATION: 420
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9000-0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 377-3231
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1403 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-908-253-3

```

	46.8%;	Score 36.5;	DB 1.	Length 1403;
46 Query Match				
	46.7%;	Pred. No. 2.4e+02;		
Best Local Similarity				
Matches	7,	Conservative	3,	Mismatches 4,
				Indels 1,
				Gaps 1.
OY	1	FAEADERDSQFPSP	IS	
	:	:		
	:			
	:			
	:			
Db	883	YARWDE-DQFPAPV	896	

```

US-08-694-865-17
US-RESULT 9
Sequence 17, Application US/08694865
Patent No. 5837268
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANN'S, JOHN G.
TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016, 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-865-17

```

	Query Match	46.8%	Score 36.5;	DB 2:	length 1403;
	Best Local Similarity	46.7%;	Pred. No.2=02;		
	Matches	7; Conservative	3; Mismatches	4; Indels	1; Gaps
OY	1 FAEDERSQPPSIP	15			
	: : : :				
Db	883 YARVD-RDQPFPAPV	896			

RESULT 10
 US-087-3
 Sequence 3, Application US/08535837
 Patent No. 5985289
 GENERAL INFORMATION:
 APPLICANT: POTTER, ANDREW A.
 APPLICANT: HARLAND, RICHARD J.
 TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
 TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ROBERTA L. ROBINS
 STREET: 285 HAMILTON AVENUE, SUITE 200
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25


```
RESULT 13
US-08-600-982-24
; Sequence 24, Application US/08600982
; Patent No. 6120991
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,982
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-8100
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1713 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: E170 protein as translated from sequence
; DESCRIPTION: of FIGURES 15A-15F, and as shown also in FIGURES
; DESCRIPTION: 19A-19R
US-08-600-982-24

Query Match          46.2%; Score 36; DB 3; Length 1713;
Best Local Similarity 77.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AADERSQ 10
    ||||:|
Db 372 AADKRESQ 380

RESULT 14
PCT-US94-10261A-24
; Sequence 24, Application PC/TUS9410261A
; GENERAL INFORMATION:
; APPLICANT: Carter, William G.
; APPLICANT: Gil, Susanna A.
; APPLICANT: Ryan, Maureen C.
; TITLE OF INVENTION: Epiligrin, an Epithelial Ligand for
; TITLE OF INVENTION: Integrins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
; STREET: 1420 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-8100
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
FILING DATE: 02-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E170 protein as translated from sequence of
DESCRIPTION: FIGURES 15A-15F, and as shown also in FIGURES 19A-19R
PCT-US94-10261A-24

Query Match          46.2%; Score 36; DB 4; Length 1713;
Best Local Similarity 77.8%; Pred. No. 3.7e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AADERSQ 10
    ||||:|
Db 372 AADKRESQ 380

RESULT 15
US-08-609-046A-2
; Sequence 2, Application US/08609046A
; Patent No. 5811298
; GENERAL INFORMATION:
; APPLICANT: RONALD DEPINHO AND NICHOLE SCHREIBER-AGUS
; TITLE OF INVENTION: REP-MAX PROTEIN HAVING ANTI-
; TITLE OF INVENTION: ONCOGENIC ACTIVITY AND USES THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,046A
; FILING DATE: FEBRUARY 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ELIZABETH A. BOGOSIAN
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: 96700/398
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION:
```

```

;
;   HYPOTHETICAL: YES
;   ANTI-SENSE: NO
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:
US-08-609-046A-2
    
```

```

Query Match      44.9%; Score 35; DB 2; Length 43;
Best Local Similarity 42.9%; Pred. No. 7.8;
Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
    
```

```

QY 1 FAADRD-----SOFPSIP 15
    | | | | |
Db 19 FLRRRECECHGYASSFPSP 39
    
```

```

Search completed: February 2, 2001, 10:36:29
Job time: 42 sec
    
```

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:35:47 ; Search time 45.64 Seconds
(without alignments)
11.238 Million cell updates/sec

Title: US-09-273-217-1

Perfect score: 78
Sequence: 1 FAFADERDSQFPSP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq.36.*
1: /SIDS1/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq/AA1985.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq/AA1986.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq/AA1987.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq/AA1988.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq/AA1989.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq/AA1990.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq/AA1991.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq/AA1992.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq/AA1993.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq/AA1994.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq/AA1995.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq/AA1996.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq/AA1997.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq/AA1998.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq/AA1999.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	15	20	V42762 Rat potassium chan
2	51	65.4	495	20	V32014 Human cation chann
3	51	65.4	858	20	V32015 Human cation chann
4	45	59.0	15	20	V42765 Rat potassium chan
5	45	57.7	532	16	R82937 Mouse Kv1.7 voltag
6	40	51.3	616	20	V32013 Drosophila melanog
7	40	51.3	1724	21	V54373 cDNA sequence enco
8	39	50.0	190	11	R03988 Mr 22k peripheral
9	39	50.0	576	20	V49541 Human PR0201 (Nsp1
10	39	50.0	576	20	V49545 Human Nsp1 mutant
11	39	50.0	576	20	V49546 Human Nsp1 mutant
12	39	50.0	576	20	V49547 Human Nsp1 mutant

13	39	50.0	576	20	Y06477 Human tumour-assoc
14	39	50.0	576	21	Y51932 Human PR0201 prote
15	39	50.0	576	21	Y51939 Human PR0201 prote
16	37	47.4	173	20	Y36238 Human secreted pro
17	37	47.4	238	21	Y99415 Human PR01410 (UNQ
18	37	47.4	438	19	W71488 Helicobacter polyp
19	37	47.4	896	13	R21580 Plasma membrane pr
20	36.5	46.8	1015	20	W97241 Protein encoded by
21	36.5	46.8	1015	20	W97243 Protein encoded by
22	36.5	46.8	1022	6	P50097 Fusion protein of
23	36.5	46.8	1076	20	Y31768 HCMV UL45-E. coli
24	36.5	46.8	1121	14	R36728 Ubiquitin fusion p
25	36.5	46.8	1199	13	R26188 HVTa antigen. Tur
26	36.5	46.8	1217	15	R49832 beat-galactosidase
27	36.5	46.8	1334	12	R14481 lKta::lacZ fusion p
28	36.5	46.8	1334	15	R50290 lKta::lacZ fusion
29	36.5	46.8	1403	12	R10890 lKta::lacZ fusion
30	36.5	46.8	1403	19	W79574 Leukotoxin 101. S
31	36	46.2	18	19	W54426 Human p5112 protel
32	36	46.2	101	20	Y29132 Amino acid sequenc
33	36	46.2	315	19	W71868 Amino acid encoded
34	36	46.2	315	19	W69384 Prostate tumour sp
35	36	46.2	315	21	Y82001 Human immunogenic
36	36	46.2	349	21	Y84617 Neisseria gonorrhoe
37	36	46.2	506	21	Y74417 Neisseria meningit
38	36	46.2	506	21	Y74418 Neisseria meningit
39	36	46.2	506	19	Y74419 Human PS112 protel
40	36	46.2	670	21	Y70229 Human RNA-associat
41	36	46.2	724	21	Y70451 Human membrane cha
42	36	46.2	1310	15	R60292 Varicella zoster v
43	36	46.2	1310	15	R55798 VZV IEP 175. Vari
44	36	46.2	1310	15	R55798 P. falciparum PREM
45	36	46.2	2228	20	W93944

ALIGNMENTS

RESULT 1	Y42762 standard; peptide; 15 AA.
ID	Y42762
XX	Y42762
AC	20-DEC-1999 (first entry)
DT	Rat potassium channel Kv1.2 vestibule-derived peptide #1.
XX	
DE	Ion channel; potassium channel; vestibule; inhibitor; antibody;
XX	polycation; antagonist; hypertension; cardiac ischaemia;
KW	bronchial constriction; neurological diseases.
XX	
OS	Synthetic.
OS	Rattus sp.
XX	
PN	W09948927-A1.
XX	
PD	30-SEP-1999.
XX	
PF	19-MAR-1999; 99WO-US06019.
XX	
PR	25-MAR-1998; 98US-0079268.
XX	
PA	(CORR) CORNELL RES FOUND INC.
XX	
PI	Huang X;
XX	
DR	WPL: 1999-601205/51.
XX	
PT	Designing specific blockers that bind to the external vestibule region
XX	of ion channels, potentially useful for treating e.g. hypertension
PS	Claim 9; Page 8; 40pp; English.

XX This sequence represents a peptide (#1), derived from the extracellular
CC vestibule portion of the rat delayed rectifier potassium channel Kv1.2.
CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
CC generate polyclonal antibodies. The vestibule portion of potassium
CC channels is located on the extracellular portion of the channel protein,
CC and generally comprises a loop between the S5 transmembrane domain and
CC the pore forming region of the channel, or between the pore forming
CC region and the S6 transmembrane domain. The antibodies generated against
CC vestibule peptides act as potassium channel inhibitors by binding to the
CC vestibule portion, physically blocking the pore, or otherwise inducing a
CC conformational change in the channel. These potassium channel blockers
CC are potential therapeutic agents for e.g., hypertension, cardiac
CC ischaemia, bronchial constriction and neurological diseases. Such
CC inhibitors are specific for particular types of ion channel, and
CC are produced by rational design based on known nucleotide and amino acid
CC sequences for ion channels.
SQ Sequence 15 AA:

Query Match 100.0%; Score 78; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEDERDSQFPSIP 15
DB 1 faeaderdsqfpsip 15
|||||

RESULT 2
Y32014
ID Y32014 standard; Protein; 495 AA.
XX Y32014;
AC Y32014;
XX 05-JAN-2000 (first entry)
DT
XX
DE Human cation channel protein.
XX
XX Cation channel protein; CCP; ion transport; arrhythmia;
KM diabetes mellitus; seizure; asthma; hypertension; therapy;
KW protein engineering; human.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Region 61..119
FT /note="crystal region"
XX
XX WO9947923-A2.
XX
XX 23-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06307.
XX
XX 20-MAR-1998; 98US-0045529.
XX 02-APR-1998; 98US-0054347.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Mackinnon R;
XX
XX WPI: 1999-601131/51.
XX
XX Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
XX
XX Claim 21; Page 135-137; 165pp; English.
XX
XX The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs

CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-22). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP in vivo, such as cardiac
CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic CCPs.
SQ Sequence 495 AA:

Query Match 65.4%; Score 51; DB 20; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.57;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEDERDSQFPSIP 15
DB 346 faeaderdsqfpsip 360
|||||

RESULT 3
Y32015
ID Y32015 standard; Protein; 858 AA.
XX Y32015;
AC Y32015;
XX 05-JAN-2000 (first entry)
DT
XX
DE Human cation channel protein.
XX
XX Cation channel protein; CCP; ion transport; arrhythmia;
KM diabetes mellitus; seizure; asthma; hypertension; therapy;
KW protein engineering; human.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Region 61..119
FT /note="crystal region"
XX
XX WO9947923-A2.
XX
XX 23-SEP-1999.
XX
XX 22-MAR-1999; 99WO-US06307.
XX
XX 20-MAR-1998; 98US-0045529.
XX 02-APR-1998; 98US-0054347.
XX
XX (UYRQ) UNIV ROCKEFELLER.
XX
XX Mackinnon R;
XX
XX WPI: 1999-601131/51.
XX
XX Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
XX
XX Claim 21; Page 137-140; 165pp; English.
XX
XX The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs.
CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-22). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP in vivo, such as cardiac

CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic CCPs.
XX
XX

SQ Sequence 858 AA;

Query Match 65.4%; Score 51; DB 20; Length 858;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADERDSQSPSIP 15
||| ||| ||| |||
Db 351 faekeddtkfsip 365

RESULT 4
Y42765
Y42765 standard; peptide: 15 AA.

AC Y42765;
DT 20-DEC-1999 (first entry)

DE Rat potassium channel Kv1.3 vestibule-derived peptide #4.

XX Ion channel; potassium channel; vestibule; inhibitor; antibody;
KW polyclonal; antagonist; hypertension; cardiac ischaemia;
KW bronchial constriction; neurological diseases.

OS Synthetic.
OS Rattus sp.

PN W09948927-A1.

PD 30-SEP-1999.

PF 19-MAR-1999; 99WO-US06019.

PR 25-MAR-1998; 98US-0079268.

PA (CORR) CORNELL RES FOUND INC.

PI Huang X;

DR WPI; 1999-601205/51.

XX Designing specific blockers that bind to the external vestibule region
XX of ion channels, potentially useful for treating e.g. hypertension -
XX
XX Claim 9; Page 9; 40pp; English.

XX This sequence represents a peptide (#4), derived from the
CC extracellular vestibule portion of the rat potassium channel Kv1.3.
CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
CC generate polyclonal antibodies. The vestibule portion of potassium
CC channels is located on the extracellular portion of the channel protein,
CC and generally comprises a loop between the S5 transmembrane domain and
CC the pore forming region of the channel, or between the pore forming
CC region and the S6 transmembrane domain. The antibodies generated against
CC vestibule peptides act as potassium channel inhibitors by binding to the
CC vestibule portion, physically blocking the pore, or otherwise inducing a
CC conformational change in the channel. These potassium channel blockers
CC are potential therapeutic agents for e.g., hypertension, cardiac
CC ischaemia, bronchial constriction and neurological diseases. Such
CC inhibitors are specific for particular types of ion channel, and
CC are produced by rational design based on known nucleotide and amino acid
XX sequences for ion channels.

SQ Sequence 15 AA;

Query Match 59.0%; Score 46; DB 20; Length 15;

Best Local Similarity 66.7%; Pred. No. 0.083;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAEADERDSQSPSIP 15
|||||: ||| |||
Db 1 faeaddptsgfsip 15

RESULT 5
R82937
R82937 standard; Protein: 532 AA.

AC R82937;

DT 10-APR-1996 (first entry)

DE Mouse Kv1.7 voltage-gated potassium channel.

XX Mouse Kv1.7 voltage-gated potassium channel;
KW insulin antagonist drug screening; insulin agonist drug screening;
KW non-insulin-dependent diabetes mellitus.

OS Mus musculus.

XX Key Location/Qualifiers

FT Domain 220..240 /note="putative membrane spanning domain (S1)"

FT Domain 286..308 /note="putative membrane spanning domain (S2)"

FT Domain 318..338 /note="putative membrane spanning domain (S3)"

FT Domain 352..372 /note="putative membrane spanning domain (S4)"

FT Domain 388..407 /note="putative membrane spanning domain (S5)"

FT Domain 449..472 /note="putative membrane spanning domain (S6)"

FT Region 421..442 /note="pore-forming region"

FT Modified-site 140..148 /note="tyrosine-kinase"

FT Modified-site 380..382 /note="protein-kinase-C"

FT Modified-site 384..386 /note="protein-kinase-C"

FT Modified-site 267 /note="potential N-glycosylation site"

PN W09523858-A1.

PD 08-SEP-1995.

PF 23-FEB-1995; 95WO-US02221.

PR 10-AUG-1994; 94US-0288405.

PR 04-MAR-1994; 94US-0207401.

PA (REGC) UNTV CALIFORNIA.

PI Chandry G, Chandry KG, Gutman GA, Kalman K;

DR WPI; 1995-320573/41.

DR N-PSDB; T04953.

XX New voltage-gated potassium channel gene - used to identify
XX material(s) which can increase insulin release e.g. for treating
XX non-insulin dependent diabetes mellitus.

PS Disclosure; Fig 1B; 38pp; English.

XX Mouse Kv1.7 is a Shaker-related voltage-gated potassium channel
CC (see Fig 1B). It may be used in drug screening for
CC identification of therapeutics which modulate the channel and,


```
XX Human Nsp1 mutant Nsp1-Y61F.
DE
DE Human; PRO201; PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; EST;
XX expressed sequence tag; tumour; tumourigenesis; diagnosis; cancer;
KW identification; proliferation; neoplastic cell growth; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX MO9954467-A1.
XX
XX 28-OCT-1999.
XX
XX 23-APR-1999; 99WO-US08847.
XX
XX 23-APR-1998; 98US-0082767.
XX
XX 22-DEC-1998; 98US-0113296.
XX
XX (GETH ) GENENTECH INC.
XX
XX Stewart TA, Lu Y;
XX
XX WPI: 1999-620728/53.
XX
XX New human polypeptides useful to screen for antagonists and produce
XX antibodies useful to diagnose and treat tumors, e.g. cancers -
XX
XX Example 4; Page 139-140; 152pp; English.
XX
XX The present invention describes human proteins designated PRO201, PRO308
XX and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
XX encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins
XX were shown to be encoded by genes that are amplified in the genome of
XX tumour cells, and are therefore believed to be useful targets for the
XX diagnosis and/or treatment (including prevention) of benign and malignant
XX tumours e.g. cancers in mammals, especially humans. They can be used to
XX produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful
XX (optionally combined with radiation treatment or a cytotoxic or
XX chemotherapeutic agent) to inhibit the growth of tumour cells or to treat
XX e.g. leukaemias, and immunologic disorders. The antibodies (especially in
XX growth inhibitory amounts) can also be included with a carrier and
XX optionally a second antibody or cytotoxic/chemotherapeutic agent in
XX compositions useful as above. They can be used to detect the proteins in
XX cells, by contacting the cell with the antibody and detecting binding,
XX useful to diagnose tumours in mammals (by contacting the antibody with a
XX tissue sample and detecting complex formation). Such diagnosis is
XX especially useful in mammals suspected of having neoplastic cell growth
XX or proliferation. The present sequence represents the human Nsp1 mutant
XX Nsp1-Y61F, which is used in an example from the present invention.
XX
XX Sequence 576 AA;
SQ
Query Match 50.0%; Score 39; DB 20; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 8 DSOFPSIP 15
| | | | | | |
Db 82 deqfslp 89
RESULT 11
ID Y49546
AC Y49546;
XX
XX 12-JAN-2000 (first entry)
XX
XX Human Nsp1 mutant Nsp1-Y95F.
DE
XX
```

```
KW Human; PRO201; PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; EST;
KW expressed sequence tag; tumour; tumourigenesis; diagnosis; cancer;
XX identification; proliferation; neoplastic cell growth; mutant.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX MO9954467-A1.
XX
XX 28-OCT-1999.
XX
XX 23-APR-1999; 99WO-US08847.
XX
XX 23-APR-1998; 98US-0082767.
XX
XX 22-DEC-1998; 98US-0113296.
XX
XX (GETH ) GENENTECH INC.
XX
XX Stewart TA, Lu Y;
XX
XX WPI: 1999-620728/53.
XX
XX New human polypeptides useful to screen for antagonists and produce
XX antibodies useful to diagnose and treat tumors, e.g. cancers -
XX
XX Example 4; Page 141-142; 152pp; English.
XX
XX The present invention describes human proteins designated PRO201, PRO308
XX and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
XX encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins
XX were shown to be encoded by genes that are amplified in the genome of
XX tumour cells, and are therefore believed to be useful targets for the
XX diagnosis and/or treatment (including prevention) of benign and malignant
XX tumours e.g. cancers in mammals, especially humans. They can be used to
XX produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful
XX (optionally combined with radiation treatment or a cytotoxic or
XX chemotherapeutic agent) to inhibit the growth of tumour cells or to treat
XX e.g. leukaemias, and immunologic disorders. The antibodies (especially in
XX growth inhibitory amounts) can also be included with a carrier and
XX optionally a second antibody or cytotoxic/chemotherapeutic agent in
XX compositions useful as above. They can be used to detect the proteins in
XX cells, by contacting the cell with the antibody and detecting binding,
XX useful to diagnose tumours in mammals (by contacting the antibody with a
XX tissue sample and detecting complex formation). Such diagnosis is
XX especially useful in mammals suspected of having neoplastic cell growth
XX or proliferation. The present sequence represents the human Nsp1 mutant
XX Nsp1-Y95F, which is used in an example from the present invention.
XX
XX Sequence 576 AA;
SQ
Query Match 50.0%; Score 39; DB 20; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 8 DSOFPSIP 15
| | | | | | |
Db 82 deqfslp 89
RESULT 12
ID Y49547
AC Y49547;
XX
XX 12-JAN-2000 (first entry)
XX
XX Human Nsp1 mutant Nsp1-Y231F.
DE
XX
XX Human; PRO201; PRO308; PRO309; Nsp1; Nsp2; Nsp3; SH2 domain; EST;
KW expressed sequence tag; tumour; tumourigenesis; diagnosis; cancer;
KW identification; proliferation; neoplastic cell growth; mutant.
```

```

XX OS Homo sapiens.
OS Synthetic.
XX PN WO9954467-A1.
XX PD 28-OCT-1999.
XX PF 23-APR-1999; 99WO-US08847.
XX PR 23-APR-1998; 98US-0082767.
XX PR 22-DEC-1998; 98US-0113296.
XX PA (GETH ) GENENTECH INC.
XX PI Stewart TA, Lu Y;
XX DR WPI, 1999-620728/53.
XX PT New human polypeptides useful to screen for antagonists and produce
XX antibodies useful to diagnose and treat tumors, e.g. cancers
XX
XX PS Example 4: Page 143-144; 152pp; English.
XX
CC The present invention describes human proteins designated PRO201, PRO308
CC and PRO309, (also designated Nsp1, Nsp2 and Nsp3 respectively) which are
CC encoded by cDNA clones DNA30676, DNA40575 and DNA61601. The proteins
CC were shown to be encoded by genes that are amplified in the genome of
CC tumor cells, and are therefore believed to be useful targets for the
CC diagnosis and/or treatment (including prevention) of benign and malignant
CC tumors e.g. cancers in mammals, especially humans. They can be used to
CC produce anti-PRO201, anti-PRO308 or anti-PRO309 antibodies useful
CC (optionally combined with radiation treatment or a cytotoxic or
CC chemotherapeutic agent) to inhibit the growth of tumour cells or to treat
CC e.g. leukemias, and immunologic disorders. The antibodies (especially in
CC growth inhibitory amounts) can also be included with a carrier and
CC optionally a second antibody or cytotoxic/chemotherapeutic agent in
CC compositions useful as above. They can be used to detect the proteins in
CC cells, by contacting the cell with the antibody and detecting binding,
CC useful to diagnose tumours in mammals (by contacting the antibody with a
CC tissue sample and detecting complex formation). Such diagnosis is
CC especially useful in mammals suspected of having neoplastic cell growth
CC or proliferation. The present sequence represents the human Nsp1 mutant
CC Nsp1-Y231F, which is used in an example from the present invention.
XX
SQ Sequence 576 AA:

```

```

Query Match 50.0%; Score 39; DB 20; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 8 DSQFSPSIP 15
   1 |11111
Db 82 deqfisp 89

```

```

RESULT 13
Y06477
ID Y06477 standard; Protein: 576 AA.
XX
AC Y06477;
XX
DT 27-SEP-1999 (first entry)
XX
DE Human tumour-associated protein PRO201.
XX
KM PRO201; UNQ175; cancer; tumour; diagnosis; therapy; human.
XX
OS Homo sapiens.
XX
PN WO9935170-A2.
XX

```

```

PD 15-JUL-1999.
XX
XX PF 05-JAN-1999; 99WO-US00106.
XX
XX PR 20-NOV-1998; 98US-0109304.
XX PR 05-JAN-1998; 98US-0070440.
XX PR 29-APR-1998; 98US-0083500.
XX PR 22-MAY-1998; 98US-0086414.
XX PR 10-JUN-1998; 98US-0088742.
XX PR 10-NOV-1998; 98US-0107783.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
XX PI Roy MA, Wood WI;
XX DR WPI, 1999-430385/36.
XX DR N-PSDB; X87254.
XX
XX PT Antibody against proteins expressed in neoplastic cells, useful for
XX tumor diagnosis and treatment
XX
XX PS Example 1; Fig 2; 162pp; English.
XX
CC This sequence represents human PRO201 (UNQ175), encoded by the
CC novel cDNA clone DNA30676 (see X87254). Amplification of DNA30676
CC occurs in various lung and colon tumours and cell lines, suggesting
CC a significant role in tumour formation and growth. Antagonists
CC (e.g. antibodies) directed against PRO201 are expected to have
CC utility in cancer therapy. The invention identifies 14 genes (see
CC X87254-67) that are amplified in the genome of tumour cells. Such
CC amplification is expected to be associated with overexpression of
CC the gene product and to contribute to tumorigenesis. The encoded
CC proteins (see Y06477-90) may be useful targets for the diagnosis
CC and/or treatment (including prevention) of certain cancers, and may
CC act as predictors of the prognosis of tumour treatment. Antibodies
CC that bind the proteins are claimed and used in claimed cancer
CC diagnostic kits.
XX
SQ Sequence 576 AA:

```

```

Query Match 50.0%; Score 39; DB 20; Length 576;
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 8 DSQFSPSIP 15
   1 |11111
Db 82 deqfisp 89

```

```

RESULT 14
Y51932
ID Y51932 standard; Protein: 576 AA.
XX
AC Y51932;
XX
DT 23-JUN-2000 (first entry)
XX
DE Human PRO201 protein.
XX
KM PRO201; human; NSP; SH2-containing protein; cytosolic; modulator;
XX Src Homology-2 containing protein; Nsp1; PRO308; Nsp2; PRO309; Nsp3;
XX cellular response; tumorigenesis; integrin stimulation; signalling.
XX
OS Homo sapiens.
XX
PN US6051403-A.
XX
PD 18-APR-2000.
XX
PF 04-AUG-1999; 99US-0369028.
XX

```

PR 23-APR-1998; 9805-0065275.
 XX (GETH) GENENTECH INC.
 XX Lu Y, Stewart TA;
 PI
 XX WPI; 2000-328246/28.
 DR N-PSDB; 289573.
 XX
 XX New isolated nucleic acid molecules encoding novel Src Homology-2
 PT containing proteins capable of modulating the activity of cellular
 PT response to external signaling -
 XX
 XX Claim 1; Column 39-44; 63pp; English.
 XX
 XX This invention describes the novel isolated Src Homology-2 (SH2)
 CC containing proteins (Nsp) (I) PRO201 (Nsp1), PRO308 (Nsp2) or PRO309
 CC (Nsp3), respectively which have cytosstatic activity. (I) plays an
 CC important role in modulating the cellular response to external stimuli.
 CC (I) binds and affects e.g. block or modulate, an activity such as
 CC regulation of tumorigenesis, response to stimulation by integrin
 CC receptors, epidermal growth factor, insulin growth factor and through
 CC other tyrosine receptor ligands, of cellular response to external
 CC signaling. (I) is useful for producing antibodies, agonists and
 CC antagonists to modulate the activity of cellular response to external
 CC signaling. The encoding Nsp nucleotides are useful as hybridization
 CC probes in chromosome and gene mapping, in cDNA library and in the
 CC generation of anti-sense RNA and DNA. They are also useful for
 CC preparing the Nsp proteins, for producing transgenic animals and for
 CC gene therapy. NI are also useful for treating and diagnosing cells
 CC associated with cell proliferative disorders. This sequence represents
 CC the PRO201 protein described in the method of the invention.
 XX
 SQ Sequence 576 AA;
 OY 8 DSOFPSIP 15
 Db 82 deqfipsip 89
 RESULT 15
 Y51939
 ID Y51939 standard; Protein; 576 AA.
 AC Y51939;
 XX
 DT 23-JUN-2000 (first entry)
 XX
 DE Human PRO201 protein.
 XX
 KW PRO201; human; Nsp; SH2-containing protein; cytosstatic; modulator;
 KM Src Homology-2 containing protein; Nsp1; PRO308; Nsp2; PRO309; Nsp3;
 XX cellular response; tumorigenesis; integrin stimulation; signaling.
 OS Homo sapiens.
 XX
 XX US6051690-A.
 PN
 PD 18-APR-2000.
 XX
 PF 23-APR-1998; 9805-0065275.
 XX
 PR 23-APR-1998; 9805-0065275.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Stewart TA, Lu Y;
 XX

DR WPI; 2000-328250/28.
 DR N-PSDB; 289585.
 XX
 PT New isolated Src Homology-2 containing polypeptides (Nsp) capable of
 PT binding and modulating cellular response to external signaling -
 XX
 XX Claim 1; Column 44-48; 63pp; English.
 XX
 XX This invention describes the novel isolated Src Homology-2 (SH2)
 CC containing proteins (Nsp) (I) PRO201 (Nsp1), PRO308 (Nsp2) or PRO309
 CC (Nsp3), respectively which have cytosstatic activity. (I) plays an
 CC important role in modulating the cellular response to external stimuli.
 CC (I) binds and affects e.g. block or modulate, an activity such as
 CC regulation of tumorigenesis, response to stimulation by integrin
 CC receptors, epidermal growth factor, insulin growth factor and through
 CC other tyrosine receptor ligands, of cellular response to external
 CC signaling. (I) is useful for producing antibodies, agonists and
 CC antagonists to modulate the activity of cellular response to external
 CC signaling. This sequence represents the PRO201 protein described in the
 CC method of the invention.
 XX
 SQ Sequence 576 AA;
 OY 8 DSOFPSIP 15
 Db 82 deqfipsip 89

Search completed: February 2, 2001, 10:38:00
 Job time: 133 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:41:47 ; Search time 20.39 Seconds
(without alignments)
23.757 Million cell updates/sec

Title: US-09-273-217-2

Sequence: 1 DPLRNXYFFDRNRPS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	495	1	CIRK1_HUMAN
2	85	100.0	495	1	CIRK1_MOUSE
3	85	100.0	495	1	CIRK1_RAT
4	85	100.0	499	1	CIRK2_HUMAN
5	85	100.0	499	1	CIRK2_MOUSE
6	85	100.0	499	1	CIRK2_XENLA
7	85	100.0	523	1	CIRK3_HUMAN
8	85	100.0	525	1	CIRK3_RAT
9	85	100.0	528	1	CIRK3_MOUSE
10	85	100.0	529	1	CIRK6_HUMAN
11	85	100.0	530	1	CIRK6_RAT
12	85	100.0	598	1	CIRK5_RABIT
13	85	100.0	601	1	CIRK5_MUSP
14	85	100.0	602	1	CIRK5_MOUSE
15	85	100.0	602	1	CIRK5_RAT
16	85	100.0	613	1	CIRK5_HUMAN
17	85	100.0	653	1	CIRK4_HUMAN
18	85	100.0	654	1	CIRK4_MOUSE
19	85	100.0	654	1	CIRK4_MOUSE
20	85	100.0	655	1	CIRK4_RAT
21	85	100.0	660	1	CIRK4_BOVIN
22	85	100.0	304	1	CIRK3_DROME
23	85	100.0	304	1	CIRK3_DROME
24	85	100.0	304	1	CIRK1_DROME
25	85	100.0	304	1	CIRK1_DROME
26	85	100.0	304	1	CIRK1_DROME
27	85	100.0	304	1	CIRK1_DROME
28	85	100.0	304	1	CIRK1_DROME
29	85	100.0	304	1	CIRK1_DROME
30	85	100.0	304	1	CIRK1_DROME
31	85	100.0	304	1	CIRK1_DROME
32	85	100.0	304	1	CIRK1_DROME
33	85	100.0	304	1	CIRK1_DROME

ALIGNMENTS

RESULT	ID	STANDARD	PRT	495 AA.
1	CIRK1_HUMAN			
AC	009470;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1 (HUK1) (HBK1).			
GN	KCNAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RA	Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,			
RA	Mathew M.K.;			
RT	"Human potassium channel genes: molecular cloning and functional			
RT	expression.";			
RL	Mol. Cell. Neurosci. 1:214-223(1990).			
RN	[2]			
RP	VARIANTS AEMK PHE-174; SER-239; ILE-249 AND ALA-408.			
RX	MEDLINE=95144169; PubMed=7842011;			
RA	Browne D.L., Gancher S.T., Nutt J.G., Brunt E.R.P., Smith E.A.,			
RA	Kramer P., Litt M.;			
RT	"Episodic ataxia/myokymia syndrome is associated with point mutations			
RT	in the human potassium channel gene, KCNAL.";			
RL	Nat. Genet. 8:136-140(1994).			
RN	[3]			
RP	VARIANTS AEMK ARG-177; ALA-226 AND ILE-404.			
RX	MEDLINE=98260872; PubMed=9600245;			
RA	Scheffer H., Brunt E.R.P., Mol G.J.J., van der Vlies P., Stulp R.P.,			
RA	Verlind E., Mantel G., Aveyanov Y.N., Holstra R.M.W., Buys C.H.C.M.;			
RT	"Three novel KCNAL mutations in episodic ataxia type I families.";			
RL	Hum. Genet. 102:464-466(1998).			
CC	-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM			
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE			
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT.			
CC	-1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLY).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE			
CC	RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE			
CC	IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL			
CC	TO SPECIFIC SUBCELLULAR COMPARTMENTS.			
CC	-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	-1- DISEASE: DEFECTS IN KCNAL ARE THE CAUSE OF MYOKYMIA WITH PERIODIC			
CC	ATAXIA (AEMK) (PAROXYSMAL OR EPISODIC ATAXIA (EA)). A DISEASE			
CC	CHARACTERIZED BY CONTINUOUS MUSCLE MOVEMENT (MYOKYMIA) AND			
CC	PERIODIC ATAXIA.			
CC	-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER			
CC	CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.			

34	42	49.4	802	1	CIRK_RAT	063099	rattus norv
35	42	49.4	806	1	CIRK_CANFA	095167	canis fami1
36	42	49.4	806	1	CIRK_HUMAN	092953	homo sapien
37	42	49.4	853	1	CIRK_RAT	P15387	rattus norv
38	42	49.4	854	1	CIRK_HUMAN	Q14721	homo sapien
39	41	48.2	221	1	SEGA_BPT4	P32286	bacterioph
40	41	48.2	525	1	WE59_LAMBD	P03754	bacterioph
41	41	48.2	757	1	CIRK_HUMAN	Q14003	homo sapien
42	41	48.2	769	1	CIRK_MOUSE	063959	mus musculu
43	41	48.2	889	1	CIRK_RAT	Q01956	rattus norv
44	40	47.1	565	1	PRIM_THEME	Q91933	thermotoga
45	40	47.1	2136	1	XCF2_MARPO	P09975	marcantaia

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation --
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announcement/
CC or send an email to license@isb-ib.ch).
CC -----
DR EMBL; L02750; AAA36139.1; -.
DR HSSP; P03621; Z1FN.
DR MIM; 176260; -.
DR MIM; 160120; -.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR PFM; PF00520; Ion_Trans; 1.
DR PRINTS; PR00169; KCANNEL.
KW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
FT Ionic channel; Transmembrane; Disease mutation.
FT TRANSEM 168 186
FT TRANSEM 221 242 SEGMENT S1 (BY SIMILARITY).
FT TRANSEM 254 274 SEGMENT S2 (BY SIMILARITY).
FT TRANSEM 290 309 SEGMENT S3 (BY SIMILARITY).
FT TRANSEM 326 345 SEGMENT S4 (BY SIMILARITY).
FT TRANSEM 387 408 SEGMENT S5 (BY SIMILARITY).
FT CARBOHYD 207 207 SEGMENT S6 (BY SIMILARITY).
FT MOD_RES 322 322 N-LINKED (GLCNAC...) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 445 445 (POTENTIAL).
FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 174 174 (POTENTIAL).
FT MOD_RES 174 174 V -> F (IN AEMK).
FT MOD_RES 177 177 /FTID-VAR_001508.
FT MOD_RES 226 226 I -> R (IN AEMK).
FT MOD_RES 239 239 /FTID-VAR_001509.
FT MOD_RES 249 249 T -> A (IN AEMK).
FT MOD_RES 249 249 /FTID-VAR_001510.
FT MOD_RES 249 249 R -> S (IN AEMK).
FT MOD_RES 249 249 /FTID-VAR_001511.
FT MOD_RES 249 249 F -> I (IN AEMK).
FT MOD_RES 249 249 /FTID-VAR_001512.
FT MOD_RES 249 249 V -> I (IN AEMK).
FT MOD_RES 249 249 /FTID-VAR_001513.
FT MOD_RES 249 249 V -> A (IN AEMK).
FT MOD_RES 249 249 /FTID-VAR_001514.
FT MOD_RES 249 249 /FTID-VAR_001515.
FT MOD_RES 249 249 /FTID-VAR_001516.
FT MOD_RES 249 249 /FTID-VAR_001517.
FT MOD_RES 249 249 /FTID-VAR_001518.
FT MOD_RES 249 249 /FTID-VAR_001519.
FT MOD_RES 249 249 /FTID-VAR_001520.
FT MOD_RES 249 249 /FTID-VAR_001521.
FT MOD_RES 249 249 /FTID-VAR_001522.
FT MOD_RES 249 249 /FTID-VAR_001523.
FT MOD_RES 249 249 /FTID-VAR_001524.
FT MOD_RES 249 249 /FTID-VAR_001525.
FT MOD_RES 249 249 /FTID-VAR_001526.
FT MOD_RES 249 249 /FTID-VAR_001527.
FT MOD_RES 249 249 /FTID-VAR_001528.
FT MOD_RES 249 249 /FTID-VAR_001529.
FT MOD_RES 249 249 /FTID-VAR_001530.
FT MOD_RES 249 249 /FTID-VAR_001531.
FT MOD_RES 249 249 /FTID-VAR_001532.
FT MOD_RES 249 249 /FTID-VAR_001533.
FT MOD_RES 249 249 /FTID-VAR_001534.
FT MOD_RES 249 249 /FTID-VAR_001535.
FT MOD_RES 249 249 /FTID-VAR_001536.
FT MOD_RES 249 249 /FTID-VAR_001537.
FT MOD_RES 249 249 /FTID-VAR_001538.
FT MOD_RES 249 249 /FTID-VAR_001539.
FT MOD_RES 249 249 /FTID-VAR_001540.
FT MOD_RES 249 249 /FTID-VAR_001541.
FT MOD_RES 249 249 /FTID-VAR_001542.
FT MOD_RES 249 249 /FTID-VAR_001543.
FT MOD_RES 249 249 /FTID-VAR_001544.
FT MOD_RES 249 249 /FTID-VAR_001545.
FT MOD_RES 249 249 /FTID-VAR_001546.
FT MOD_RES 249 249 /FTID-VAR_001547.
FT MOD_RES 249 249 /FTID-VAR_001548.
FT MOD_RES 249 249 /FTID-VAR_001549.
FT MOD_RES 249 249 /FTID-VAR_001550.
FT MOD_RES 249 249 /FTID-VAR_001551.
FT MOD_RES 249 249 /FTID-VAR_001552.
FT MOD_RES 249 249 /FTID-VAR_001553.
FT MOD_RES 249 249 /FTID-VAR_001554.
FT MOD_RES 249 249 /FTID-VAR_001555.
FT MOD_RES 249 249 /FTID-VAR_001556.
FT MOD_RES 249 249 /FTID-VAR_001557.
FT MOD_RES 249 249 /FTID-VAR_001558.
FT MOD_RES 249 249 /FTID-VAR_001559.
FT MOD_RES 249 249 /FTID-VAR_001560.
FT MOD_RES 249 249 /FTID-VAR_001561.
FT MOD_RES 249 249 /FTID-VAR_001562.
FT MOD_RES 249 249 /FTID-VAR_001563.
FT MOD_RES 249 249 /FTID-VAR_001564.
FT MOD_RES 249 249 /FTID-VAR_001565.
FT MOD_RES 249 249 /FTID-VAR_001566.
FT MOD_RES 249 249 /FTID-VAR_001567.
FT MOD_RES 249 249 /FTID-VAR_001568.
FT MOD_RES 249 249 /FTID-VAR_001569.
FT MOD_RES 249 249 /FTID-VAR_001570.
FT MOD_RES 249 249 /FTID-VAR_001571.
FT MOD_RES 249 249 /FTID-VAR_001572.
FT MOD_RES 249 249 /FTID-VAR_001573.
FT MOD_RES 249 249 /FTID-VAR_001574.
FT MOD_RES 249 249 /FTID-VAR_001575.
FT MOD_RES 249 249 /FTID-VAR_001576.
FT MOD_RES 249 249 /FTID-VAR_001577.
FT MOD_RES 249 249 /FTID-VAR_001578.
FT MOD_RES 249 249 /FTID-VAR_001579.
FT MOD_RES 249 249 /FTID-VAR_001580.
FT MOD_RES 249 249 /FTID-VAR_001581.
FT MOD_RES 249 249 /FTID-VAR_001582.
FT MOD_RES 249 249 /FTID-VAR_001583.
FT MOD_RES 249 249 /FTID-VAR_001584.
FT MOD_RES 249 249 /FTID-VAR_001585.
FT MOD_RES 249 249 /FTID-VAR_001586.
FT MOD_RES 249 249 /FTID-VAR_001587.
FT MOD_RES 249 249 /FTID-VAR_001588.
FT MOD_RES 249 249 /FTID-VAR_001589.
FT MOD_RES 249 249 /FTID-VAR_001590.
FT MOD_RES 249 249 /FTID-VAR_001591.
FT MOD_RES 249 249 /FTID-VAR_001592.
FT MOD_RES 249 249 /FTID-VAR_001593.
FT MOD_RES 249 249 /FTID-VAR_001594.
FT MOD_RES 249 249 /FTID-VAR_001595.
FT MOD_RES 249 249 /FTID-VAR_001596.
FT MOD_RES 249 249 /FTID-VAR_001597.
FT MOD_RES 249 249 /FTID-VAR_001598.
FT MOD_RES 249 249 /FTID-VAR_001599.
FT MOD_RES 249 249 /FTID-VAR_001600.
FT MOD_RES 249 249 /FTID-VAR_001601.
FT MOD_RES 249 249 /FTID-VAR_001602.
FT MOD_RES 249 249 /FTID-VAR_001603.
FT MOD_RES 249 249 /FTID-VAR_001604.
FT MOD_RES 249 249 /FTID-VAR_001605.
FT MOD_RES 249 249 /FTID-VAR_001606.
FT MOD_RES 249 249 /FTID-VAR_001607.
FT MOD_RES 249 249 /FTID-VAR_001608.
FT MOD_RES 249 249 /FTID-VAR_001609.
FT MOD_RES 249 249 /FTID-VAR_001610.
FT MOD_RES 249 249 /FTID-VAR_001611.
FT MOD_RES 249 249 /FTID-VAR_001612.
FT MOD_RES 249 249 /FTID-VAR_001613.
FT MOD_RES 249 249 /FTID-VAR_001614.
FT MOD_RES 249 249 /FTID-VAR_001615.
FT MOD_RES 249 249 /FTID-VAR_001616.
FT MOD_RES 249 249 /FTID-VAR_001617.
FT MOD_RES 249 249 /FTID-VAR_001618.
FT MOD_RES 249 249 /FTID-VAR_001619.
FT MOD_RES 249 249 /FTID-VAR_001620.
FT MOD_RES 249 249 /FTID-VAR_001621.
FT MOD_RES 249 249 /FTID-VAR_001622.
FT MOD_RES 249 249 /FTID-VAR_001623.
FT MOD_RES 249 249 /FTID-VAR_001624.
FT MOD_RES 249 249 /FTID-VAR_001625.
FT MOD_RES 249 249 /FTID-VAR_001626.
FT MOD_RES 249 249 /FTID-VAR_001627.
FT MOD_RES 249 249 /FTID-VAR_001628.
FT MOD_RES 249 249 /FTID-VAR_001629.
FT MOD_RES 249 249 /FTID-VAR_001630.
FT MOD_RES 249 249 /FTID-VAR_001631.
FT MOD_RES 249 249 /FTID-VAR_001632.
FT MOD_RES 249 249 /FTID-VAR_001633.
FT MOD_RES 249 249 /FTID-VAR_001634.
FT MOD_RES 249 249 /FTID-VAR_001635.
FT MOD_RES 249 249 /FTID-VAR_001636.
FT MOD_RES 249 249 /FTID-VAR_001637.
FT MOD_RES 249 249 /FTID-VAR_001638.
FT MOD_RES 249 249 /FTID-VAR_001639.
FT MOD_RES 249 249 /FTID-VAR_001640.
FT MOD_RES 249 249 /FTID-VAR_001641.
FT MOD_RES 
```

RT	"A famlly of three mouse potassium channel genes with intronless coding regions."
RL	Science 247:973-975(1990).
RN	(2)
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE=88189348; PubMed=2451788;
RA	Tempel B.L., Jan Y.N., Jan L.Y.;
RL	"Cloning of a probable potassium channel gene from mouse brain.";
CC	Nature 332:837-839(1988).
CC	-I FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC	-I SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC	-I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-I DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC	-I DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC	-I SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUPERFAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M30439; AAA39711.1; -;
DR	EMBL; Y00305; CABA68408.1; -;
DR	PIR; S06378; S06378.
DR	PIR; A40090; A40090.
DR	HSSP; P03621; ZIFN.
MD	MGI:96654; KCNAL.
DR	INTERPRO; IPRO00636; -;
DR	INTERPRO; IPRO03091; -;
DR	Pfam; PF00520; Ion_trans; 1.
DR	PRINTS; PR00169; KCHANNEL.
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Multigene family; Phosphorylation.
FT	TRANSMEM 168 186 SEGMENT S1.
FT	TRANSMEM 221 242 SEGMENT S2.
FT	TRANSMEM 254 274 SEGMENT S3.
FT	TRANSMEM 290 309 SEGMENT S4.
FT	TRANSMEM 326 345 SEGMENT S5.
FT	TRANSMEM 387 408 SEGMENT S6.
FT	CARBOHYD 207 207 N-LINKED (GLCNAC...) (POTENTIAL).
FT	MOD_RES 322 322 PHOSPHORYLTATION (BY CAPK)
FT	MOD_RES 446 446 PHOSPHORYLTATION (BY CAPK)
FT	POSHORYLTATION (BY CAPK) (POTENTIAL).
SO	SEQUENCE 495 AA; 56409 MW; C9249FI30E943D3D CRC66;
QY	Query Match 100.0%; Score 85; DB 1; Length 495; Best Local Similarity 100.0%; Pred. No. 2.6e-07; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 DPLRNEYFFDRNRPS 15 74 DPLRNEYFFDRNRPS 88
RESULT	3
SIK1_RAT	

ID CIRK1_RAT STANDARD; PRT: 495 AA.
AC P10499;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (1A) (RBK1) (RCK1).
GN KCNA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-89052659; PubMed-3191911;
RA Baumann A., Grube A., Ackermann A., Pongs O.;
RT "Structure of the voltage-dependent potassium channel is highly
RT conserved from Drosophila to vertebrate central nervous systems";
RL EMBO J. 7:2457-2463(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-89203264; PubMed-2539643;
RA Christie M.J., Adelman J.P., Douglass J., North R.A.;
RT "Expression of a cloned rat brain potassium channel in Xenopus
RT oocytes";
RL Science 244:221-224(1989).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12589; CAA31102.1; -;
DR EMBL: M26161; AAA41982.1; -;
DR PIR: A41353; A41353.
DR PIR: S01161; S01161.
DR HSP: P03621; 21FN.
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR003091; -;
DR PFA: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 367 408 SEGMENT S6.
FT CAROHD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)

FT SQ SEQUENCE 495 AA; 56379 MW; 29804463133F5D31 CRC64; (POTENTIAL).
Query Match 100.0%; Score 85; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DPLRNEFFEDRRNPS 15
DB 74 DPLRNEFFEDRRNPS 88
RESULT 4
CIRK2_HUMAN STANDARD; PRT: 499 AA.
AC P16389;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (HBK5) (NGK1)
DE (MK2) (HUKIV).
GN KCNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RA Mathew M.K.;
RT "Human potassium channel genes: molecular cloning and functional
RT expression";
RL Mol. Cell. Neurosci. 1:214-223(1990).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L02752; AAA36141.1; -;
DR HSP: P03621; 21FN.
DR MIM: 176262; -;
DR INTERPRO: IPR000636; -;
DR INTERPRO: IPR003091; -;
DR PFA: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.

```

FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT SEQUENCE 499 AA; 56716 MW; 4B03F1B46A826C39 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2,6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEYFEDRRNPS 15
Db 70 DPLRNEYFEDRRNPS 84

RESULT 5
CIRK2_MOUSE STANDARD; PRT; 499 AA.
ID CIRK2_MOUSE 002010;
AC P15386; 002010;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (RBK2) (RCK5) (NGK1)
DE (MK2) (HUKIV).
GN KCNA2.
OS Mus musculus (Mouse), and Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE-89255260; PubMed-2722779;
RA McKinnon D.;
RT "Isolation of a cDNA clone coding for a putative second potassium
channel indicates the existence of a gene family."
RL J. Biol. Chem. 264:8230-8236(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT; TISSUE-BRAIN;
RX MEDLINE-90059914; PubMed-2555158;
RA Stuehrmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
Stoecker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
RT "Molecular basis of functional diversity of voltage-gated potassium
channels in mammalian brain."
RL EMBO J. 8:3235-3244(1989).
RN [3]
RP REVISIONS.
RA Ludwig J.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-RAT;
RX MEDLINE-91352097; PubMed-1715584;
RA Paulmichl M., Nasmitz P., Herlitz R., Reed K., Boyle W.A.,
Nerbonne J.M., Peralta E.G., Clapham D.E.;
RT "Cloning and expression of a rat cardiac delayed rectifier potassium
channel."
RL Proc. Natl. Acad. Sci. U.S.A. 88:7892-7895(1991).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-MOUSE;
RX MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
Ghanshani S., Tempel B.L., Gutman G.A.;
RT "A family of three mouse potassium channel genes with intronless
coding regions."
RL Science 247:973-975(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

```

```

CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROPENTAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J04731; AAA40819.1; -
DR EMBL; X16003; CAA34134.1; -
DR EMBL; M74449; AAL19867.1; -
DR EMBL; M30440; AAA39713.1; -
DR PIR; A33814; A33814.
DR PIR; S06709; S06709.
DR PIR; B40090; B40090.
DR HSSP; P03621; 21FN.
DR MGD; MGI:96659; KCNA2.
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR003091; -
DR PRAM; PR00520; ion.trans. 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1.
FT TRANSMEM 222 243 SEGMENT S2.
FT TRANSMEM 255 275 SEGMENT S3.
FT TRANSMEM 293 311 SEGMENT S4.
FT TRANSMEM 328 347 SEGMENT S5.
FT TRANSMEM 389 411 SEGMENT S6.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT SEQUENCE 499 AA; 56700 MW; A8FEA6F3F59AFA2A CRC64;
SQ CONFLICT 411 411 S -> F (IN REF. 4).
FT SEQUENCE 499 AA; 56700 MW; A8FEA6F3F59AFA2A CRC64;

Query Match 100.0%; Score 85; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2,6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEYFEDRRNPS 15
Db 70 DPLRNEYFEDRRNPS 84

RESULT 6
CIRK2_XENLA STANDARD; PRT; 499 AA.
ID CIRK2_XENLA 002739;
AC P22739;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.2 (XSHN2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

```

[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=91026051; PubMed=2223094;
RA Ribera A.B.;
RT "A potassium channel gene is expressed at neural induction.";
RL Neuron 5:691-701(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M35664; AAA49933.1; -
DR PIR: JH0313; JH0313.
DR HSSP: P03621; 21FN.
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion.trans: 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT FT TRANSMEM 164 182 SEGMENT S1.
FT FT TRANSMEM 222 243 SEGMENT S2.
FT FT TRANSMEM 255 275 SEGMENT S3.
FT FT TRANSMEM 293 311 SEGMENT S4.
FT FT TRANSMEM 328 347 SEGMENT S5.
FT FT TRANSMEM 389 411 SEGMENT S6.
FT FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK)
FT FT (POTENTIAL).
SQ SEQUENCE 499 AA; 56701 MW; 11415768038DCBB CRC64;
Query Match 100.0%; Score 85; DB 1; Length 499;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84
RESULT 7
CIR3_HUMAN STANDARD: PRT; 523 AA.
AC P22001;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL3 (HPCN3) (HGK5) (HUKI11)
DE (HUK3).
GN KCNA3 OR HGK5.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKELTAL MUSCLE;
RX MEDLINE=91095456; PubMed=198682;
RA Phillips L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
RA Nelson D.J., Steiner D.F.;
RT "Sequence and functional expression in Xenopus oocytes of a human
RT insulinoma and islet potassium channel.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPHOCYTES;
RX MEDLINE=92189730; PubMed=1547020;
RA Cal Y.-C., Osborne P.B., North R.A., Doolley D.C., Douglass J.;
RT "Characterization and functional expression of genomic DNA encoding
RT the human lymphocyte type n potassium channel.";
RL DNA Cell Biol. 11:163-172(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92235098; PubMed=1373731;
RA Attali B., Romey G., Honore E., Schmid-Alliana A., Mattei M.-G.,
RA Lesage F., Ricard P., Barhanin J., Lazdunski M.;
RT "Cloning, functional expression, and regulation of two K+ channels in
RT human T lymphocytes.";
RL J. Biol. Chem. 267:8650-8657(1992).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=95130104; PubMed=7829094;
RA Polander K., Douglass J., Swanson R.;
RT "Confirmation of the assignment of the gene encoding Kv1.3, a
RT voltage-gated potassium channel (KCNA3) to the proximal short arm of
RT human chromosome 1.";
RL Genomics 23:295-296(1994).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HEPTEPENTAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M5515; AAA36425.1; -
DR EMBL: M38217; AAB88073.1; -
DR EMBL: M85217; AAA59457.1; -
DR EMBL: L23499; AAC31761.1; -
DR HSSP: P03621; 21FN.
DR MIM: 176263; -
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion.trans: 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 183 201 SEGMENT S1.
 FT TRANSMEM 243 264 SEGMENT S2.
 FT TRANSMEM 276 296 SEGMENT S3.
 FT TRANSMEM 311 329 SEGMENT S4.
 FT TRANSMEM 346 365 SEGMENT S5.
 FT TRANSMEM 407 429 SEGMENT S6.
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 468 468 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CONFLICT 20 20 A -> G (IN REF. 1).
 FT CONFLICT 37 37 L -> V (IN REF. 1).
 FT CONFLICT 61 61 L -> V (IN REF. 3).
 FT CONFLICT 91 91 L -> V (IN REF. 1).
 FT CONFLICT 257 257 E -> K (IN REF. 4).
 FT CONFLICT 338 338 T -> S (IN REF. 1).
 FT CONFLICT 419 419 S -> T (IN REF. 1).
 FT CONFLICT 488 488 S -> T (IN REF. 1).
 SQ SEQUENCE 523 AA; 58303 MW; 8BA2PLC7C802B411 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 523;
 Best Local Similarity 100.0%; Pred. No. 2.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
 |||||
 DB 89 DPLRNEYFFDRNRPS 103

RESULT 8
 ID CIK3_RAT STANDARD; PRT; 525 AA.
 AC P15384;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (RGK5) (RCK3) (KV3).
 GN KCNA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-90059914; PubMed-2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroetter K.H., Sakmann B.,
 RT Stocker M., Glese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";

RL EMO J. 8:3235-3244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-90287965; PubMed-2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOCYTES;
 RX MEDLINE-90278098; PubMed-2351830;
 RA Douglass J., Osborne P.B., Cai Y.C., Wilkinson M., Christie M.J.,
 RA Adelman J.P.;
 RT "Characterization and functional expression of a rat genomic DNA
 RT clone encoding a lymphocyte potassium channel.";
 RL J. Immunol. 144:4841-4850(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL: X16001; CAA34132.1; -;
 DR EMBL: M30312; AAA42035.1; -;
 DR EMBL: M31744; AAA41500.1; -;
 DR PIR: S06708; S06708.
 DR PIR: JH0168; JH0168.
 DR HSSP: P03621; ZIFN.
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR0003091; -;
 DR PFAM: PF00520; Ion_trans. 1.
 DR PRINTS: PR00169; KCHANNEL.

KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 185 203 SEGMENT S1.
 FT TRANSMEM 245 266 SEGMENT S2.
 FT TRANSMEM 278 298 SEGMENT S3.
 FT TRANSMEM 313 331 SEGMENT S4.
 FT TRANSMEM 348 367 SEGMENT S5.
 FT TRANSMEM 409 431 SEGMENT S6.
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 470 470 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT CONFLICT 106 106 F -> L (IN REF. 1).
 FT CONFLICT 181 181 G -> R (IN REF. 3).
 FT CONFLICT 430 430 V -> L (IN REF. 3).
 SQ SEQUENCE 525 AA; 58424 MW; 6DA8869D5471C401 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 525;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
 |||||
 DB 91 DPLRNEYFFDRNRPS 105

RESULT 9
 ID CIK3_MOUSE STANDARD; PRT; 528 AA.
 AC P16350;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (MK3).
 GN KCNA3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA Ghanshani S., Tempel B.L., Gutan G.A.;
RT "A family of three mouse potassium channel genes with intronless
RT coding regions.";
RL Science 247:973-975(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL; M30441; AAA39716.1; -.
DR HSSP; P03621; 2IFN.
DR MGD; MGI:96660; KCNAB3.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR PFAM; PF00520; Ion_trans.1.
DR PRINTS; PR00169; KCHANNEL.
DR KMW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 188 206 SEGMENT S1.
FT TRANSMEM 248 269 SEGMENT S2.
FT TRANSMEM 281 301 SEGMENT S3.
FT TRANSMEM 316 334 SEGMENT S4.
FT TRANSMEM 351 370 SEGMENT S5.
FT TRANSMEM 412 434 SEGMENT S6.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 473 473 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 473 473 (POTENTIAL).
SQ SEQUENCE 528 AA; 58526 MW; CDB5F1515F9A731 CRC64;

```

Query Match 100.0%; Score 85; DB 1; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFEDNRPS 15
|||||
DB 94 DPLRNEYFEDNRPS 108

RESULT 10
CIR6_HUMAN STANDARD; PRT; 529 AA.
ID CIR6_HUMAN
AC P17658;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

```

DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.6 (HBR2).
GN KCNAB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE-BRAIN;
RX MEDLINE-90269208; PubMed-2347305;
RA Grube A., Schroeter K.H., Ruppersberg J.P., Stocker M., Drewes T.,
RA Becht S., Pongs O.;
RT "Cloning and expression of a human voltage-gated potassium channel. A
RT novel member of the RCK potassium channel family.";
RL EMBL J. 9:1749-1756(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL; X17622; CAA55623.1; -.
DR PIR; S15057; S15057.
DR MIM; 176257; -.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR003091; -.
DR PFAM; PF00520; Ion_trans.1.
DR PRINTS; PR00169; KCHANNEL.
DR KMW Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 175 193 SEGMENT S1.
FT TRANSMEM 263 284 SEGMENT S2.
FT TRANSMEM 296 316 SEGMENT S3.
FT TRANSMEM 340 360 SEGMENT S4.
FT TRANSMEM 376 396 SEGMENT S5.
FT TRANSMEM 437 457 SEGMENT S6.
FT MOD_RES 511 511 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 511 511 (PROBABLE).
SQ SEQUENCE 529 AA; 58728 MW; CFF0710A1E9CD69F CRC64;

```

Query Match 100.0%; Score 85; DB 1; Length 529;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFEDNRPS 15
|||||
DB 78 DPLRNEYFEDNRPS 92

RESULT 11
CIR6_RAT STANDARD; PRT; 530 AA.
ID CIR6_RAT
AC P17659; P19025;
DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, last sequence update)
 DT 13-JUL-1998 (Rel. 36, last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.6 (RCK2) (KV2).
 GN KCVNA6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN CORTEX;
 RX MEDLINE=90269208; PubMed=2347305;
 RA Grupe A., Schroeter K.H., Ruppertsberg J.P., Stocker M., Drewes T.,
 RA Beckh S., Pongs O.;
 RT "Cloning and expression of a human voltage-gated potassium channel. A
 RT novel member of the RCK potassium channel family.";
 RL EMBO J. 9:1749-1756(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=90297965; PubMed=2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Polander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=91105598; PubMed=1993474;
 RA Kirsch G.E., Drewe J.A., Verna S., Brown A.M., Joho R.H.;
 RT "Electrophysiological characterization of a new member of the RCK
 RT family of rat brain K⁺ channels.";
 RL FEBS Lett. 278:55-60(1991).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X17621; CAA35622.1; -;
 DR EMBL: M27159; AAA41499.1; ALT_SEQ.
 DR PIR: JH0167; JH0167.
 DR PIR: S12786; S12786.
 DR INTERPRO: IPR000636; -;
 DR PIR: PFO0520; IPR003091; -;
 DR PIR: PFO0520; IPR003091; -;
 DR PRINTS: PRO0169; KCHANEL.
 KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 175 193 SEGMENT S1.
 FT TRANSMEM 264 285 SEGMENT S2.
 FT TRANSMEM 297 317 SEGMENT S3.
 FT TRANSMEM 341 361 SEGMENT S4.

FT TRANSMEM 377 397 SEGMENT S5.
 FT TRANSMEM 438 458 SEGMENT S6.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 222 222 PHOSPHORYLATION (BY CK2) (POTENTIAL).
 FT MOD_RES 512 512 PHOSPHORYLATION (BY CKAP)
 FT MOD_RES 528 528 (PROBABLE).
 FT MOD_RES 528 528 PHOSPHORYLATION (BY CAPK)
 FT CONFLICT 241 241 (POTENTIAL).
 FT CONFLICT 333 333 S -> L (IN REF. 3).
 FT CONFLICT 333 333 R -> G (IN REF. 2).
 SO SEQUENCE 530 AA; 58883 MW; 30A9774B66C1DA5 CRC64;
 Query Match 100.0%; Score 85; DB 1; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2,8e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DPLRNEYFFDRNRPS 15
 DB 78 DPLRNEYFFDRNRPS 92
 AC P50638;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL.5.
 GN KCVNA5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JAPANESE WHITE; TISSUE-HEART;
 RX MEDLINE=96032538; PubMed=7556635;
 RA Sasaki Y., Ishii K., Nunoki K., Yamagishi T., Taira N.;
 RT "The voltage-dependent K⁺ channel (Kvl.5) cloned from rabbit heart
 RT and facilitation of inactivation of the delayed rectifier current by
 RT the rat beta subunit.";
 RL FEBS Lett. 372:20-24(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NEW ZEALAND WHITE; TISSUE-PORTAL VEIN;
 RA Clement-Chomienne O., Ishii K., Walsh M.P., Cole W.C.;
 RT "Rabbit portal vein Kvl.5.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROQUATERNARY OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@sib-sib.ch.

CC EMBL: D45025; BAA08082.1; -
CC EMBL: AF036943; AAC13312.1; -
CC HSSP: P03621; 2IFN.
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
KM Ionic channel; Multigene family; Phosphorylation.
FT TRANSMEM 235 253 SEGMENT S1.
FT TRANSMEM 310 330 SEGMENT S2.
FT TRANSMEM 341 362 SEGMENT S3.
FT TRANSMEM 383 404 SEGMENT S4.
FT TRANSMEM 419 440 SEGMENT S5.
FT TRANSMEM 480 501 SEGMENT S6.
FT DOMAIN 78 83 POLY-GLY.
FT DOMAIN 367 372 POLY-GLY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 598 AA; 65475 MW; B06D235ACTA8E1F0 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEYFDRNRPS 15
Db 141 DPLRNEYFDRNRPS 155

RESULT 13
CIR5_MOUSE
ID CIR5_MOUSE STANDARD; PRT: 601 AA.
AC P79197;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5.
GN KCNA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=HEART ATRIUM;
RA Schwiegel T., Polander K., Swanson R.;
RL Submitted (Jan-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@sib-sib.ch.

CC EMBL: U45979; ABA41145.1; -
CC INTERPRO: IPR000636; -
CC INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
KM Ionic channel; Multigene family; Phosphorylation.
FT TRANSMEM 240 258 SEGMENT S1.
FT TRANSMEM 314 334 SEGMENT S2.
FT TRANSMEM 345 366 SEGMENT S3.
FT TRANSMEM 386 407 SEGMENT S4.
FT TRANSMEM 422 443 SEGMENT S5.
FT TRANSMEM 483 504 SEGMENT S6.
FT DOMAIN 370 375 POLY-GLY.
FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 601 AA; 65889 MW; 14ZDB9F8CB843FE0 CRC64;

Query Match 100.0%; Score 85; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DPLRNEYFDRNRPS 15
Db 146 DPLRNEYFDRNRPS 160

RESULT 14
CIR5_MOUSE
ID CIR5_MOUSE STANDARD; PRT: 602 AA.
AC Q61762;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5 (KVL1-5).
GN KCNA5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS; TISSUE=HEART;
RX MEDLINE=94043264; PubMed=8226976;
RA Attali B., Lesage F., Ziliani P., Guillemare E., Honore E.,
RA Walzmann R., Hugnot J.-P., Mattei M.-G., Lazdunski M., Barhanin J.;
RT "Multiple mRNA isoforms encoding the mouse cardiac Kvl-1.5 delayed
RT rectifier K+ channel.";
RL J. Biol. Chem. 268:24283-24289(1993).
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS: KVL1-5 (SHOWN HERE), KVL1-5/5',
CC AND KVL1-5/3'; ARE PRODUCED BY ALTERNATIVE SPLICING. KVL1-5/3' IS
CC NON-FUNCTIONAL BUT INHIBITS EXPRESSION OF KVL1-5.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND MODERATELY
CC IN BRAIN. LOW LEVELS IN THYMUS, SKELETAL MUSCLE AND SPLEEN. NOT
CC EXPRESSED IN LIVER, LUNG OR KIDNEY.
CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER

CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L22218; AAA39365.1; -
CC DR HSSP: P03621; 21FN.
CC DR MGD; MGI:96662; KCNA5.
CC DR INTERPRO; IPR000636; -
CC DR PFM; PF00520; Ion_trans; 1.
CC DR PRINTS; PRO0169; KCHANEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation;
CC KW Alternative splicing.
CC FT TRANSMEM 242 260 SEGMENT S1.
CC FT TRANSMEM 316 336 SEGMENT S2.
CC FT TRANSMEM 347 368 SEGMENT S3.
CC FT TRANSMEM 387 408 SEGMENT S4.
CC FT TRANSMEM 423 444 SEGMENT S5.
CC FT TRANSMEM 484 505 SEGMENT S6.
CC FT DOMAIN 373 376 POLY-GLY.
CC FT CARBOHYD 44 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
CC FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT VARSPLIC 1 200 MISSING (IN ISOFORM KVI-5/3').
CC FT VARSPLIC 515 602 MISSING (IN ISOFORM KVI-5/3').
CC SQ SEQUENCE 602 AA; 66644 MW; FC2C92E8062FAC97 CRC64;
Query Match 100.0%; Score 85; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFFDRNRP 15
Db 148 DPLRNEYFFDRNRP 162
RESULT 15
CIRK5_RAT
ID CIRK5_RAT STANDARD; PRT; 602 AA.
AC P19024;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVI.5 (KVI) (RCK7).
GN KCNA5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-90297965; PubMed-2361015;
RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
RA Bennett C., Stein R.B., Kaczmarek L.M.;
RT "Cloning and expression of cDNA and genomic clones encoding three
RT delayed rectifier potassium channels in rat brain."
RL Neuron 4:929-939(1990).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M27158; AAA41498.1; -
CC DR PTR; JH0166; JH0166.
CC DR HSSP; P03621; 21FN.
CC DR INTERPRO; IPR000636; -
CC DR INTERPRO; IPR003091; -
CC DR PFM; PF00520; Ion_trans; 1.
CC DR PRINTS; PRO0169; KCHANEL.
CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation;
CC FT TRANSMEM 242 260 SEGMENT S1.
CC FT TRANSMEM 316 336 SEGMENT S2.
CC FT TRANSMEM 347 368 SEGMENT S3.
CC FT TRANSMEM 387 408 SEGMENT S4.
CC FT TRANSMEM 423 444 SEGMENT S5.
CC FT TRANSMEM 484 505 SEGMENT S6.
CC FT DOMAIN 373 376 POLY-GLY.
CC FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT MOD_RES 81 81 PHOSPHORYLATION (BY CK2) (POTENTIAL).
CC FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC SQ SEQUENCE 602 AA; 66552 MW; 6A784535FF226ED7 CRC64;
Query Match 100.0%; Score 85; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFFDRNRP 15
Db 148 DPLRNEYFFDRNRP 162

Search completed: February 2, 2001, 10:41:47
Job time: 311 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:39:07 ; Search time 62.83 Seconds
(without alignments)
27.982 Million cell updates/sec

Title: US-09-273-217-2

Perfect score: 85

Sequence: 1 DPLRNEYFDRNRPS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	476	6	Q08635
2	85	100.0	483	13	Q09PM8
3	85	100.0	483	13	Q01829
4	85	100.0	489	13	Q01781
5	85	100.0	499	6	Q0MYX3
6	85	100.0	515	5	Q16968
7	85	100.0	522	5	Q01335
8	85	100.0	529	11	Q01923
9	85	100.0	583	11	Q09XX0
10	85	100.0	593	6	Q02848
11	85	100.0	597	6	Q09TS07
12	85	100.0	602	11	Q021R6
13	85	100.0	662	13	Q09YGX8
14	82	96.5	516	6	Q02856
15	80	94.1	359	5	Q04277
16	80	94.1	708	5	Q09VM29
17	77	90.6	512	5	Q026597
18	75	88.2	511	4	Q016322
19	75	88.2	725	6	Q028649

20	73	85.9	488	5	Q05376	Q05376	Loligo opal
21	72	84.7	494	13	Q01830	Q01830	oncorhynchu
22	68	80.0	499	6	Q02893	Q02893	canis fam11
23	58	68.2	301	5	Q05071	Q05071	haemacoba
24	58	68.2	532	11	Q070259	Q070259	mus musculu
25	57	67.1	556	5	Q017535	Q017535	caenorhabdi
26	57	67.1	558	5	Q062350	Q062350	caenorhabdi
27	55	64.7	489	5	Q026041	Q026041	panulirus i
28	54	63.5	206	5	Q076778	Q076778	haemopis ma
29	54	63.5	452	5	Q076266	Q076266	hirudo medi
30	54	63.5	484	5	Q022012	Q022012	caenorhabdi
31	54	63.5	514	5	Q07457	Q07457	aplysia cal
32	54	63.5	518	5	Q09YIC6	Q09YIC6	drosophila
33	54	63.5	776	5	Q019464	Q019464	caenorhabdi
34	49	57.6	500	4	Q090HJ4	Q090HJ4	homo sapien
35	49	57.6	503	11	P97557	P97557	rattus norv
36	49	57.6	504	11	Q060565	Q060565	mesocricetu
37	49	57.6	545	2	Q08159	Q08159	shigella fl
38	49	57.6	4226	5	Q0989H5	Q0989H5	plasmodium
39	46	54.1	323	5	Q001800	Q001800	caenorhabdi
40	45	52.9	487	5	Q026094	Q026094	poliorchis
41	45	52.9	670	5	Q077270	Q077270	drosophila
42	44	51.8	496	3	Q04919	Q04919	saccharomyc
43	44	51.8	1024	3	Q074889	Q074889	schizosacch
44	43.5	51.2	518	13	Q073606	Q073606	gallus gall
45	43	50.6	63	6	Q09TV14	Q09TV14	oryctolagus

ALIGNMENTS

```

RESULT 1
ID Q08635 PRELIMINARY: PRT: 476 AA.
AC Q08635;
AD 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN KVL.2 (BKs) (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92267180; PubMed=1587348;
RA Reid P.F., Pongs O., Dolly J.O.;
RT *Cloning of a bovine voltage-gated K+ channel gene utilizing partial
RT amino acid sequence of a dendrotoxin-binding protein from brain
RT cortex.*;
RL FEBS Lett. 302:31-34(1992).
CC CC
CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -I- SIMILARITY: BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC COMPARTMENTS.
CC EMBL: X66185; CAA46953.1; -.
CC INTERPRO: IPR000636; -.
CC INTERPRO: IPR001622; -.
CC INTERPRO: IPR003091; -.
CC INTERPRO: IPR003191; -.
CC PFM: PFM00520; ion.trans; 1.
CC PFM: PFM02214; K.tetra; 1.

```

DR PRINTS: PR00169; KCHANNEL.
KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycophorin; Multigene family; Phosphorylation.
FT TRANSMEM 164 182 SEGMENT S1 (BY SIMILARITY).
FT TRANSMEM 222 243 SEGMENT S2 (BY SIMILARITY).
FT TRANSMEM 255 275 SEGMENT S3 (BY SIMILARITY).
FT TRANSMEM 293 311 SEGMENT S4 (BY SIMILARITY).
FT TRANSMEM 328 347 SEGMENT S5 (BY SIMILARITY).
FT TRANSMEM 389 411 SEGMENT S6 (BY SIMILARITY).
FT MOD_RES 449 449 PHOSPHORYLATION (BY CAPK).
FT CARBOHYD 38 38 (BY SIMILARITY).
FT CARBOHYD 207 207 POTENTIAL.
FT NON_TER 476 476 POTENTIAL.
SQ SEQUENCE 476 AA; 54152 MW; D350456A611C057D CRC64;

Query Match 100.0%; Score 85; DB 6; Length 476;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84
|||||

RESULT 2
Q9PWW8 PRELIMINARY; PRT; 483 AA.
AC Q9PWW8:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE POTASSIUM CHANNEL SHAKER ALPHA SUBUNIT VARIANT CKV1.4(W).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=INNER EAR;
RA Rajeevan M.S., Hu S., Sakai Y., Sokolowski B.H.A.;
RT "Cloning and expression of Shaker alpha and beta subunits during inner ear development."
RL Brain Res. Mol. Brain Res. 66:83-93(1999).
DR EMBL: AF084460; AD17794.1; -.
DR HSSP: P15385; 12TO.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 483 AA; 54289 MW; 394855F1A2F73366 CRC64;

Query Match 100.0%; Score 85; DB 13; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 229 DPLRNEYFFDRNRPS 243
|||||

RESULT 3
Q91829 PRELIMINARY; PRT; 483 AA.
AC Q91829:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE SHAKER-RELATED POTASSIUM CHANNEL TSH2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98146169; PubMed=9486764;
RA Nguyen T.D., Jeserich G.;
RT "Molecular structure and expression of shaker type potassium channels in glial cells of trout CNS."
RL J. Neurosci. Res. 51:284-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Nguyen T.D., Jeserich G.;
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252302; AAF70088.1; -.
KW Ionic channel.
SQ SEQUENCE 483 AA; 54955 MW; 68A78AEC4424956 CRC64;

Query Match 100.0%; Score 85; DB 13; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 71 DPLRNEYFFDRNRPS 85
|||||

RESULT 4
Q91781 PRELIMINARY; PRT; 489 AA.
AC Q91781:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE POTASSIUM CHANNEL.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LARYNGEAL MUSCLE;
RX MEDLINE=94045927; PubMed=8229210;
RA Ribeiro A.B., Nguyen D.A.;
RT "Primary sensory neurons express a Shaker-like potassium channel gene."
RL J. Neurosci. 13:4988-4996(1993).
DR EMBL: M94258; AAA16340.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 489 AA; 55995 MW; 5C5DD41334D58A43 CRC64;

Query Match 100.0%; Score 85; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 1 DPLRNEYFFDRNRPS 15
|||||

Db 71 DPLRNEYFDRNRPS 85

RESULT 5

ID Q9MYX3 PRELIMINARY; PRT; 499 AA.

AC Q9MYX3; TREMBLrel. 15, Created.
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE POTASSIUM CHANNEL SUBUNIT KV 1.2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCB1_Taxid=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Thorndeloe K.S., Walsh M.P., Cole W.C.;
 RT "Rabbit portal vein Kv 1.2."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF284420; AAF91476.1; --
 SQ SEQUENCE 499 AA; 56692 MW; 7A4BF46D8FB36308 CRC64;

Query Match 100.0%; Score 85; DB 6; Length 499;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
 DB 70 DPLRNEYFDRNRPS 84

RESULT 6
 ID Q16968 PRELIMINARY; PRT; 515 AA.

AC Q16968; TREMBLrel. 01, Created.
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspiidea;
 OC Aplysiidae; Aplysia.
 OX NCB1_Taxid=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91186212; PubMed=2010814;
 RA Pfaffinger P.J., Furukawa Y., Zhao B., Dugan D., Kandel E.R.;
 RT "Cloning and expression of an Aplysia K+ channel and comparison with
 native Aplysia K+ currents."
 RL J. Neurosci. 11:918-927(1991).
 DR EMBL: M95914; AAA2756.1; --
 DR INTERPRO: IPR000636; --
 DR INTERPRO: IPR001622; --
 DR INTERPRO: IPR003091; --
 DR INTERPRO: IPR003131; --
 DR PFM: PF00520; Ion_trans; 1.
 DR PFM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 515 AA; 58539 MW; 76F6579C4C4D91E4 CRC64;

Query Match 100.0%; Score 85; DB 5; Length 515;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
 DB 103 DPLRNEYFDRNRPS 117

RESULT 7

ID O61335 PRELIMINARY; PRT; 522 AA.

AC O61335; TREMBLrel. 07, Created.
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL.
 GN SHAER.
 OS Panulirus interruptus (California spiny lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
 OC Palinuroidea; Palinuridae; Panulirus.
 OX NCB1_Taxid=6735;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97477441; PubMed=9334397;
 RA Kim M., Baro D.J., Lanning C.C., Doshi M., Farnham J., Moskowitz H.S.,
 RA Peck J.H., Olivera B.M., Harris-Warrick R.M.;
 RT "Alternative splicing in the pore-forming region of shaker potassium
 channels."
 RT J. Neurosci. 17:8213-8224(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kim M.T., Baro D.J., Lanning C.C., Doshi M., Moskowitz H., Farnham J.,
 RA Harris-Warrick R.M.;
 RL Recept. Channels 0:0-0(1998).
 DR EMBL: AF017129; AAC05909.1; --
 DR INTERPRO: IPR000636; --
 DR INTERPRO: IPR001622; --
 DR INTERPRO: IPR003091; --
 DR INTERPRO: IPR003131; --
 DR PFM: PF00520; Ion_trans; 1.
 DR PFM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 522 AA; 59513 MW; 0FF0E7B233A33FBD CRC64;

Query Match 100.0%; Score 85; DB 5; Length 522;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
 DB 91 DPLRNEYFDRNRPS 105

RESULT 8
 ID O61923 PRELIMINARY; PRT; 529 AA.

AC O61923; TREMBLrel. 01, Created.
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MURINE POTASSIUM CHANNEL PROTEIN.
 GN MKL.6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCB1_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Migeon M.B., Street V.A., Demas V.P., Tempel B.L.;
 RL Epilepsy Res. 0:0-0(0).
 DR EMBL: M96688; AAA39772.1; --
 DR INTERPRO: IPR000636; --
 DR INTERPRO: IPR001622; --
 DR INTERPRO: IPR003091; --
 DR INTERPRO: IPR003131; --
 DR PFM: PF00520; Ion_trans; 1.
 DR PFM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel.
SQ SEQUENCE 529 AA; 58673 MW; 336D78C069ABEADD CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 11; Length 529;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 78 DPLRNEYFFDRNRPS 92

RESULT 9
Q9XXX0 ID Q9XXX0 PRELIMINARY; PRT; 583 AA.
AC Q9XXX0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE TUKVI.
GN Halocynthia roretzi (Sea squirt).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729; [1]
RP SEQUENCE FROM N.A.
RA Ono F., Katayama Y., Nakajo K., Okamura Y.;
RT "Distinct mechanism controlling Na and K channel expression in a
developing neuronal blastomere."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020853; BAA78383.1; -
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -
DR PFAM: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
SQ SEQUENCE 583 AA; 65935 MW; D9D00B42373B7EFD CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 5; Length 583;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 103 DPLRNEYFFDRNRPS 117

RESULT 10
Q28248 ID Q28248 PRELIMINARY; PRT; 593 AA.
AC Q28248;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE DELAYED RECTIFIER K+ CHANNEL (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615; [1]
RN SEQUENCE FROM N.A.
RC TISSUE-COLON.
RA Overurf K.E., Russell S.N., Carl A., Vogalis R., Hart P.J.,
RL Hume J.R., Sanders K.M., Horowitz B.;
AM J. Physiol. 267:0-0(1994).
DR EMBL; U08596; AAA57320.1; -
DR HSSP; O54397; 1BL8.
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -

DR INTERPRO: IPR003131; -
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
FT NON_TER 593
SQ SEQUENCE 593 AA; 65617 MW; 056278731409B228 CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 6; Length 593;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 143 DPLRNEYFFDRNRPS 157

RESULT 11
Q9TS07 ID Q9TS07 PRELIMINARY; PRT; 597 AA.
AC Q9TS07;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE BAK5-DELAYED RECTIFIER POTASSIUM CHANNEL KV1.5 HOMOLOG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913; [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=95046327; PubMed=7957920;
RA Garcia-Guzman M., Sala F., Criado M., Sala S.;
RT "A delayed rectifier potassium channel cloned from bovine adrenal
medulla. Functional analysis after expression in Xenopus oocytes and
in a neuroblastoma cell line."
RL FEBS Lett. 354:173-176(1994).
DR INTERPRO: IPR000636; -
DR INTERPRO: IPR001622; -
DR INTERPRO: IPR003091; -
DR INTERPRO: IPR003131; -
DR PFAM: PF00520; Ion_trans; 1.
DR PFAM: PF02214; K_tetra; 1.
DR PRINTS: PR00169; KCHANNEL.
SQ SEQUENCE 597 AA; 65757 MW; DE55DF1B767C20A CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 6; Length 597;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 142 DPLRNEYFFDRNRPS 156

RESULT 12
Q9ZIR6 ID Q9ZIR6 PRELIMINARY; PRT; 602 AA.
AC Q9ZIR6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE VENTRICULAR POTASSIUM CHANNEL KV1.5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090; [1]
RN SEQUENCE FROM N.A.
RP Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark B., Giles W.R.;


```

RT "Cloning and functional expression of mouse heart K+ channel alpha-
RT subunits, Kv1.5, Kv4.2, and Kv4.3."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF108659; AAD13779.1; -.
DR HSSP; Q54397; 1BL8.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR001622; -.
DR INTERPRO; IPR003091; -.
DR INTERPRO; IPR003131; -.
DR PFAM; PF00520; Ion_trans; 1.
DR PFAM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
KM Ionic channel.
SQ SEQUENCE 602 AA; 66579 MW; 02926E85DC022DDA CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 11; Length 602;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 148 DPLRNEYFFDRNRPS 162

RESULT 13
Q9YGX8 PRELIMINARY; PRT; 662 AA.
ID Q9YGX8;
AC Q9YGX8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL SHAKER CKV1.4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99197209; PubMed-10095080;
RA Raleevan M.S., Hu S., Sakai Y., Sokolowski B.H.A.;
RT "Cloning and expression of Shaker alpha- and beta-subunits during
RT inner ear development."
RL Brain Res. Mol. Brain Res. 66:83-93(1999).
DR EMBL; U82365; AAD11454.1; -.
DR HSSP; P15385; 1ZTO.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR001622; -.
DR INTERPRO; IPR003091; -.
DR INTERPRO; IPR003131; -.
DR PFAM; PF00520; Ion_trans; 1.
DR PFAM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
KM Ionic channel.
SQ SEQUENCE 662 AA; 74061 MW; 7DB994240DF58007 CRC64;

Query Match
Best Local Similarity 100.0%; Score 85; DB 13; Length 662;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 229 DPLRNEYFFDRNRPS 243

RESULT 14
Q28656 PRELIMINARY; PRT; 516 AA.
ID Q28656;
AC Q28656;
DT 01-NOV-1998 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

```

```

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE GLIBENCLAMIDE-SENSITIVE VOLTAGE-GATED POTASSIUM CHANNEL.
GN Kv1.3-GLVB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RX MEDLINE=96249424; PubMed=8647945;
RA Yao X., Chang A.Y., Boulpaep E.L., Segal A.S., Desir G.V.;
RT "Molecular cloning of a glibenclamide-sensitive, voltage-gated
RT potassium channel expressed in rabbit kidney."
RL J. Clin. Invest. 97:2525-2533(1996).
DR EMBL; U38240; AAC24718.1; -.
DR HSSP; Q54397; 1BL8.
DR INTERPRO; IPR000636; -.
DR INTERPRO; IPR001622; -.
DR INTERPRO; IPR003091; -.
DR INTERPRO; IPR003131; -.
DR PFAM; PF00520; Ion_trans; 1.
DR PFAM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
KM Ionic channel.
SQ SEQUENCE 516 AA; 57430 MW; 795E84998BCA7CAA CRC64;

Query Match
Best Local Similarity 96.5%; Score 82; DB 6; Length 516;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 82 DPLRNEYFFDRNRPS 96

RESULT 15
Q24277 PRELIMINARY; PRT; 359 AA.
ID Q24277;
AC Q24277;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (FRAGMENT).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87273502; PubMed=2440582;
RA Kamb A., Iverson L.E., Tanouye M.A.;
RT "Molecular characterization of Shaker, a Drosophila gene that encodes
RT a potassium channel."
RL Cell 50:405-413(1987).
DR EMBL; M17155; AAA70217.1; -.
DR FLYBASE; FBgn0003380; Sh.
DR INTERPRO; IPR003091; -.
DR INTERPRO; IPR003131; -.
DR PFAM; PF02214; K_tetra; 1.
DR PRINTS; PR00169; KCHANNEL.
KM Ionic channel; Membrane.
FT NON_TER 1
FT NON_TER 359
SQ SEQUENCE 359 AA; 42622 MW; C1380CECC4512A70 CRC64;

Query Match
Best Local Similarity 94.1%; Score 80; DB 5; Length 359;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:37:10 ; Search time 38.22 Seconds
(without alignments)
26.649 Million cell updates/sec

Title: US-09-273-217-2

Perfect score: 85

Sequence: 1 DPLRNEYFFDRNRPS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	476	2 S21144	potassium channel
2	85	100.0	489	2 I51532	potassium channel
3	85	100.0	495	2 I57680	potassium channel
4	85	100.0	495	2 A40090	potassium channel
5	85	100.0	495	2 B39113	potassium channel
6	85	100.0	499	2 JH0313	potassium channel
7	85	100.0	499	2 I77466	potassium channel
8	85	100.0	499	2 I84204	potassium channel
9	85	100.0	499	2 A33814	potassium channel
10	85	100.0	514	2 C49507	potassium channel
11	85	100.0	523	2 A38101	potassium channel
12	85	100.0	523	2 I52990	voltage-gated pota
13	85	100.0	525	2 A43531	potassium channel
14	85	100.0	528	2 I84205	potassium channel
15	85	100.0	529	2 S12787	potassium channel
16	85	100.0	530	2 JH0167	potassium channel
17	85	100.0	597	2 S51212	BAK5 protein - bov
18	85	100.0	598	2 S66669	potassium channel
19	85	100.0	602	2 A49507	potassium channel
20	85	100.0	602	2 JH0166	potassium voltage-
21	85	100.0	613	2 A56031	potassium channel
22	85	100.0	653	2 A39922	potassium channel
23	85	100.0	654	2 S11049	potassium channel
24	85	100.0	654	2 E39113	potassium channel
25	85	100.0	660	2 S24125	potassium channel
26	80	94.1	304	2 S02284	potassium channel
27	80	94.1	349	2 S00482	potassium channel
28	80	94.1	359	2 A27159	potassium channel
29	80	94.1	564	2 S01110	potassium channel

30	80	94.1	616	2 S00479	potassium channel
31	80	94.1	643	2 S00480	potassium channel
32	80	94.1	656	2 JH0193	potassium channel
33	68	80.0	499	2 A48672	delayed rectifier
34	57	67.1	558	2 T23991	hypothetical prote
35	55	64.7	489	2 JC4787	shaw protein - Cal
36	55	64.7	498	2 A41359	potassium channel
37	55	64.7	498	2 S12748	potassium channel
38	54	63.5	484	2 T24238	hypothetical prote
39	54	63.5	776	2 T20896	hypothetical prote
40	46	54.1	323	2 T29032	hypothetical prote
41	45	52.9	670	2 T13739	probable hormone r
42	44	51.8	1024	2 T41415	probable leucine p
43	44	51.8	1323	2 A24534	regulatory protein
44	43	50.6	460	2 T27759	hypothetical prote
45	43	50.6	511	2 A46020	potassium channel

ALIGNMENTS

```
RESULT 1
S21144
potassium channel protein RCK5 - bovine (fragment)
N:Alternate names: potassium channel protein 2
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Nov-1993 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C:Accession: S21144; A23668; A33158
R:Reid, P.F.; Pongs, O.; Dolly, J.O.
FEBS Lett. 302, 31-34, 1992
A>Title: Cloning of a bovine voltage-gated K(+) channel gene utilising partial amino
A:Reference number: S21144; MUID:92267180
A:Accession: S21144
A:Molecule type: DNA
A:Residues: 1-476 <REI>
A:Cross-references: GB:X66185; NID:q395206; PIDN:CA446953.1; PID:q395207
A>Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 320-
R:Scott, V.E.S.; Pearce, D.N.; Keen, J.N.; Findlay, J.B.C.; Dolly, J.O.
J. Biol. Chem. 265, 20094-20097, 1990
A>Title: alpha-Dendrotoxin acceptor from bovine brain is a K(+) channel protein. Evid
A:Reference number: A23668; MUID:91056043
A:Accession: A23668
A:Molecule type: protein
A:Residues: 2-28 <SCO>
R:Newitt, R.A.; Houamed, K.M.; Rehm, H.; Tempel, B.L.
submitted to the Protein Sequence Database, February 1991
A:Reference number: A33158
A:Accession: A33158
A:Molecule type: protein
A:Residues: 2-27 <NEW>
C:Keywords: glycoprotein; transmembrane protein
F:38,207,466/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
Db 70 DPLRNEYFFDRNRPS 84

RESULT 2
I5132
potassium channel - african clawed frog
C:Species: Xenopus laevis (african clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I5132
R:Ribera, A.B.; Nguyen, D.A.
J. Neurosci. 13, 4988-4996, 1993
A>Title: Primary sensory neurons express a Shaker-like potassium channel gene.
A:Reference number: I5132; MUID:94045927
```

A:Accession: I51532
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-489 <RIB>
A:Cross-references: GB:M94258; NID:g387892; PIDN:AAA16340.1; PID:g387893

Query Match 100.0%; Score 85; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 71 DPLRNEYFFDRNRPS 85

RESULT 3
157680
potassium channel KCNA1 - human
N:Alternate names: potassium channel protein HRC-1
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
C:Accession: I57680; A60173
R:Ramashwami, M.; Gautam, M.; Kamp, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
Mol. Cell. Neurosci. 1, 214-223, 1990
A:Title: Human potassium channel genes: molecular cloning and functional expression.
A:Reference number: I57680
A:Accession: I57680
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-495 <RMB>
A:Cross-references: GB:L02750; NID:g186662; PIDN:AAA3139.1; PID:g186663
R:Freeman, S.N.; Conley, E.C.; Brennand, J.C.; Russell, N.J.W.; Brammar, W.J.
Biochem. Soc. Trans. 18, 891a, 1990
A:Title: Cloning and characterization of a cDNA encoding a human brain potassium channel.
A:Reference number: A60173; MUID:91192386
A:Accession: A60173
A:Molecule type: mRNA
A:Residues: 263-264, 266-314, 'R' <PRE>
C:Genetics:
A:Gene: GDB:KCNA1; RBK1; HUK1; MBK1; AEMK; KVL1.1
A:Cross-references: GDB:127903; OMIM:176260
A:Map position: 12p13-12p13

Query Match 100.0%; Score 85; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 74 DPLRNEYFFDRNRPS 88

RESULT 4
A40090
potassium channel KVL1.1 protein - mouse
N:Alternate names: potassium channel A; potassium channel MK1
C:Species: Mus musculus (house mouse)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999
C:Accession: A40090; S06376; I60746
R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanashanl, S.; Tempel, B.L.
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regions.
A:Reference number: A40090; MUID:90161996
A:Accession: A40090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <CHA>
A:Cross-references: GB:M30439; NID:g199702; PIDN:AAA39711.1; PID:g199703
R:Tempel, B.L.; Jan, Y.N.; Jan, L.Y.
Nature 332, 837-839, 1988
A:Title: Cloning of a probable potassium channel gene from mouse brain.

A:Reference number: S06378; MUID:88189348
A:Accession: S06378
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-495 <TEM>

A:Cross-references: GB:Y00305; GB:M36456; NID:g53605; PIDN:CAA68408.1; PID:g53606
A:Note: It is uncertain whether Met-1 or Met-4 is the initiator
C:Genetics:
A:Gene: MBK1; MK1
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:361-370/Domain: transmembrane beta strand #status predicted <TMB1>
F:371-379/Domain: transmembrane beta strand #status predicted <TMB2>
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 74 DPLRNEYFFDRNRPS 88

RESULT 5
B39113
potassium channel KVL1.1 - rat
N:Alternate names: potassium channel A; potassium channel RK1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 05-Nov-1999
C:Accession: B39113; A41353; S01161
R:Roberts, S.L.; Tamkun, M.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
A:Title: Cloning and tissue-specific expression of five voltage-gated potassium channels.
A:Reference number: A39113; MUID:91156694
A:Accession: B39113
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-495 <ROB>
R:Christie, M.J.; Adelman, J.P.; Douglass, J.; North, R.A.
Science 244, 221-224, 1989
A:Title: Expression of a cloned rat brain potassium channel in Xenopus oocytes.
A:Reference number: A41353; MUID:89203264
A:Accession: A41353
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-495 <CHR>
R:Baumann, A.; Grube, A.; Ackermann, A.; Pongs, O.
EMBO J. 7, 2457-2463, 1988
A:Title: Structure of the voltage-dependent potassium channel is highly conserved from
A:Reference number: S01161; MUID:89052659
A:Accession: S01161
A:Molecule type: mRNA
A:Residues: 1-495 <BAU>
A:Cross-references: EMBL:X12589; NID:g55957; PIDN:CAA1102.1; PID:g55958
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:361-370/Domain: transmembrane beta strand #status predicted <TMB1>
F:371-379/Domain: transmembrane beta strand #status predicted <TMB2>
F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 85; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 6.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 74 DPLRNEYFFDRNRPS 88

RESULT 6
JH0313

potassium channel protein XShaz - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: JH0313
 R:Ribera, A.B.
 Neuron 5, 691-701, 1990
 A:Title: A potassium channel gene is expressed at neural induction.
 A:Reference number: JH0313; MUID:91026051
 A:Accession: JH0313
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-499 <RIB>

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
 |||
 Db 70 DPLRNEYFFDRNRPS 84

RESULT 7
 177466
 potassium channel - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: 177466
 R:Ramseyhaml, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.
 Mol. Cell. Neurosci. 1, 214-223, 1990
 A:Title: Human potassium channel genes: molecular cloning and functional expression.
 A:Reference number: 157680
 A:Accession: 177466
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-499 <RES>
 A:Cross-references: GB:L02752; NID:9186668; PIDN:AAA36141.1; PID:9186669

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
 |||
 Db 70 DPLRNEYFFDRNRPS 84

RESULT 8
 184204
 potassium channel protein MK2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: B40090; 184204
 R:Chandry, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanshani, S.; Tempel, B.L.
 Science 247, 973-975, 1990
 A:Title: A family of three mouse potassium channel genes with intronless coding regions.
 A:Reference number: A40090; MUID:90161996
 A:Accession: B40090
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-499 <CHA>
 A:Cross-references: GB:M30440; NID:9199706; PIDN:AAA39713.1; PID:9199707
 C:Genetics:
 A:Gene: MK2

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15

Db 70 DPLRNEYFFDRNRPS 84
 |||

RESULT 9
 A33814
 potassium channel Kv1.2 - rat
 M:Alternate names: potassium channel RCK5; potassium channel RK2; RAK
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 05-Nov-1999
 C:Accession: A33814; C39113; S06709; I59204
 R:McKinnon, D.
 J. Biol. Chem. 264, 8230-8236, 1989
 A:Title: Isolation of a cDNA clone coding for a putative second potassium channel ind
 A:Reference number: A33814; MUID:89255260
 A:Accession: A33814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-499 <MCK>

A:Cross-references: GB:J04731; NID:9203154; PIDN:AAA40819.1; PID:9203155
 R:Roberds, S.L.; Tamkun, M.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991
 A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chann
 A:Reference number: A39113; MUID:91156694
 A:Accession: C39113
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-12,24-499 <ROB>
 R:Stuhmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Glese,
 EMBO J. 8, 3235-3244, 1989
 A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
 A:Reference number: S06708; MUID:90059914
 A:Accession: S06709
 A:Molecule type: mRNA
 A:Residues: 1-247,'SC',250-261,'T',263-282,'HTNR',288-291,'T',293-499 <STU>
 A:Cross-references: EMBL:X16003
 R:Paulmichl, M.; Nasmith, P.; Hellmisse, R.; Reed, K.E.; Boyle, W.A.; Nerbonne, J.M.;
 Proc. Natl. Acad. Sci. U.S.A. 88, 7892-7895, 1991
 A:Title: Cloning and expression of a rat cardiac delayed rectifier potassium channel.
 A:Reference number: I59204; MUID:91352097
 A:Accession: I59204
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-410,'F',412-499 <RES>
 A:Cross-references: GB:M74449; NID:9206548; PIDN:AAA19867.1; PID:9206549
 A:Experimental source: heart atrium
 C:Genetics:
 A:Gene: RAK

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
 F:164-182/Domain: transmembrane #status predicted <TM1>
 F:222-243/Domain: transmembrane #status predicted <TM2>
 F:255-275/Domain: transmembrane #status predicted <TM3>
 F:288-311/Domain: transmembrane #status predicted <TM4>
 F:328-347/Domain: transmembrane #status predicted <TM5>
 F:363-372/Domain: transmembrane beta strand #status predicted <TM1>
 F:373-381/Domain: transmembrane beta strand #status predicted <TM2>
 F:389-411/Domain: transmembrane beta strand #status predicted <TM2>
 F:207/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:449/Binding site: phosphate (ser) (covalent) (by CAMP-dependent kinase) #status pre

Query Match 100.0%; Score 85; DB 2; Length 499;
 Best Local Similarity 100.0%; Pred. No. 6.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
 |||
 Db 70 DPLRNEYFFDRNRPS 84

RESULT 10
 C49507
 potassium channel Kv1.5, form 3 - mouse

C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: C49507
R:Altali, B.; Lesage, F.; Zilliani, P.; Guillemare, E.; Honore, E.; Walldmann, R.; Hugnot, J. Biol. Chem. 268, 24283-24289, 1993
A:Title: Multiple mRNA isoforms encoding the mouse cardiac Kv1-5 delayed rectifier K(+) A:Reference number: A49507; MUID:94043264
A:Accession: C49507
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <ATT>
A:Cross-references: GB:L22218
C:Keywords: alternative splicing

Query Match 100.0%; Score 85; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEFFDRRPS 15
Db 148 DPLRNEFFDRRPS 162

RESULT 11
A38101
potassium channel KCNA3 - human
N:Alternate names: potassium channel HK3; potassium channel PCN3; shaker-related potass
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-1999
C:Accession: A38101; B38556
R:Altali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Mattei, M.G.; Lesage, F.; Ricar
J. Biol. Chem. 267, 8650-8657, 1992
A:Title: Cloning, functional expression, and regulation of two K(+) channels in human T
A:Reference number: A38101; MUID:92235098
A:Accession: A38101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-523 <ATT>
A:Cross-references: GB:M85217; NID:q186664; PIDN:AAA59457.1; PID:q186665
R:Phillipson, L.H.; Hlce, R.E.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Nelson, D.J.; St
Proc. Natl. Acad. Sci. U.S.A. 88, 53-57, 1991
A:Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma and
A:Reference number: A38556; MUID:91095456
A:Accession: B38556
A:Molecule type: DNA
A:Residues: 1-19, 'G', 21-36, 'V', 38-60, 'L', 62-90, 'V', 92-337, 'S', 339-418, 'S', 420-457, 'LS', 4
A:Cross-references: GB:M55515
C:Genetics:
A:Gene: GDB:KCNA3
A:Cross-references: GDB:128079; OMIM:176263
A:Map position: 1p21-1p13.3
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 100.0%; Score 85; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEFFDRRPS 15
Db 89 DPLRNEFFDRRPS 103

RESULT 12
I52990
voltage-gated potassium channel - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52990
R:Cal, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
DNA Cell Biol. 11, 163-172, 1992
A:Title: Characterization and functional expression of genomic DNA encoding the human 1y

A:Reference number: I52990; MUID:92189730
A:Accession: I52990
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-523 <RES>
A:Cross-references: GB:M38217; NID:q186670; PIDN:AAA88073.1; PID:q186671
C:Genetics:
A:Gene: HGKS

Query Match 100.0%; Score 85; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEFFDRRPS 15
Db 89 DPLRNEFFDRRPS 103

RESULT 13
A43531
potassium channel Kv1.3 - rat
N:Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel R
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 05-Nov-1999
C:Accession: A43531; JH0168; S06708
R:Douglass, J.; Osborne, P.B.; Cal, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P
J. Immunol. 144, 4841-4850, 1990
A:Title: Characterization and functional expression of a rat genomic DNA clone encodi
A:Reference number: A43531; MUID:90278098
A:Accession: A43531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-525 <DOU>
A:Cross-references: GB:M30312
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.;
Neuron 4, 929-939, 1990
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rec
A:Reference number: JH0166; MUID:90297965
A:Accession: JH0168
A:Molecule type: DNA
A:Residues: 1-180, 'G', 182-525 <SMA>
A:Cross-references: GB:M31744; NID:q205104; PIDN:AAA41500.1; PID:q205105
A:Experimental source: brain
A:Note: only a list of differences from sequence S06708 is given
R:Stuehmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese,
EMBO J. 8, 3235-3244, 1989
A:Title: Molecular basis of functional diversity of voltage-gated potassium channels
A:Reference number: S06708; MUID:90059914
A:Accession: S06708
A:Molecule type: mRNA
A:Residues: 1-105, 'L', 107-180, 'G', 182-525 <STU>
A:Cross-references: EMBL:X16001; NID:q57034; PIDN:CAA34132.1; PID:q57035
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:185-203/Domain: transmembrane #status predicted <TM1>
F:245-266/Domain: transmembrane #status predicted <TM2>
F:278-298/Domain: transmembrane #status predicted <TM3>
F:313-331/Domain: transmembrane #status predicted <TM4>
F:348-367/Domain: transmembrane #status predicted <TM5>
F:383-392/Domain: transmembrane beta strand #status predicted <TM6>
F:393-401/Domain: transmembrane beta strand #status predicted <TM7>
F:409-431/Domain: transmembrane #status predicted <TM8>
F:470/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pre

RESULT 14

184205

potassium channel protein MK3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C:Accession: C40090; 184205

R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Chanshani, S.; Tempel, B.L

Science 247, 973-975, 1990

A>Title: A family of three mouse potassium channel genes with intronless coding regions.

A:Reference number: A40090; MUID:90161996

A:Accession: C40090

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-528 <CH>

A:Cross-references: GB:M30441; NID:g199712; PID:AAA39716.1; PID:g199713

Query Match 100.0%; Score 85; DB 2; Length 528;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15

|||||

DB 94 DPLRNEYFFDRNRPS 108

RESULT 15

S12787

potassium channel KCNA2 - human

N:Alternate names: potassium channel HBK2

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999

C:Accession: S12787; S15057

R:Grube, A.; Schroeter, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.; Por

EMBO J. 9, 1749-1756, 1990

A>Title: Cloning and expression of a human voltage-gated potassium channel. A novel mem

A:Reference number: S12786; MUID:90269208

A:Accession: S12787

A:Molecule type: mRNA

A:Residues: 1-529 <GRU>

A:Cross-references: EMBL:X17622

R:Pongs, O.

submitted to the EMBL Data Library, November 1989

A:Reference number: S15057

A:Accession: S15057

A:Molecule type: mRNA

A:Residues: 1-57, 'T', '59-529 <PON>

A:Cross-references: EMBL:X17622; NID:g32032; PID:CAA35623.1; PID:g32033

C:Genetics:

A:Gene: GDB:KCNK2; HK4; KY1.2

A:Cross-references: GDB:128062; OMIM:176262

C:Keywords: glycoprotein; ion channel; transmembrane protein

F:175-193/Domain: transmembrane #status predicted <TM1>

F:263-284/Domain: transmembrane #status predicted <TM2>

F:296-316/Domain: transmembrane #status predicted <TM3>

F:340-358/Domain: transmembrane #status predicted <TM4>

F:376-395/Domain: transmembrane #status predicted <TM5>

F:437-458/Domain: transmembrane #status predicted <TM6>

Query Match 100.0%; Score 85; DB 2; Length 529;

Best Local Similarity 100.0%; Pred. No. 7.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15

|||||

DB 78 DPLRNEYFFDRNRPS 92

Search completed: February 2, 2001, 10:37:11
Job time: 84 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:29 ; Search time 34.98 Seconds
(without alignments)
7.700 Million cell updates/sec

Title: US-09-273-217-2

Sequence: 1 DPLRNEYFFDRNRPS 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	149	2	US-08-606-143-24
2	85	100.0	150	2	US-08-606-143-26
3	85	100.0	150	2	US-08-606-143-29
4	85	100.0	151	2	US-08-606-143-19
5	85	100.0	152	2	US-08-606-143-4
6	85	100.0	152	2	US-08-606-143-5
7	85	100.0	152	2	US-08-606-143-6
8	85	100.0	152	2	US-08-606-143-7
9	85	100.0	152	2	US-08-606-143-9
10	85	100.0	152	2	US-08-606-143-10
11	85	100.0	152	2	US-08-606-143-12
12	85	100.0	152	2	US-08-606-143-13
13	85	100.0	152	2	US-08-606-143-15
14	85	100.0	152	2	US-08-606-143-16
15	85	100.0	152	2	US-08-606-143-18
16	85	100.0	152	2	US-08-606-143-20
17	85	100.0	152	2	US-08-606-143-21
18	85	100.0	152	2	US-08-606-143-25
19	85	100.0	152	2	US-08-606-143-30
20	85	100.0	152	2	US-08-606-143-32
21	85	100.0	153	2	US-08-606-143-11
22	85	100.0	153	2	US-08-606-143-22
23	85	100.0	153	2	US-08-606-143-27
24	85	100.0	153	2	US-08-606-143-31
25	85	100.0	155	2	US-08-606-143-8
26	85	100.0	155	2	US-08-606-143-14
27	85	100.0	155	2	US-08-606-143-17
28	85	100.0	155	2	US-08-606-143-23

29	85	100.0	528	2	US-08-527-152-2	Sequence 2, Appl
30	82	96.5	152	2	US-08-606-143-28	Sequence 28, Appl
31	58	68.2	532	1	US-08-288-405A-10	Sequence 10, Appl
32	43	50.6	200	2	US-08-606-143-42	Sequence 42, Appl
33	43	50.6	513	4	US-08-464-340A-2	Sequence 2, Appl
34	43	50.6	513	4	PCT-US94-08449A-2	Sequence 2, Appl
35	42	49.4	179	2	US-08-606-143-33	Sequence 33, Appl
36	42	49.4	179	2	US-08-606-143-34	Sequence 34, Appl
37	42	49.4	179	2	US-08-606-143-35	Sequence 35, Appl
38	42	49.4	179	2	US-08-606-143-36	Sequence 36, Appl
39	42	49.4	539	1	US-08-464-340A-13	Sequence 13, Appl
40	41	48.2	190	2	US-08-606-143-37	Sequence 37, Appl
41	41	48.2	208	2	US-08-606-143-40	Sequence 40, Appl
42	40	47.1	494	1	US-08-464-340A-4	Sequence 4, Appl
43	40	47.1	494	4	PCT-US94-08449A-4	Sequence 4, Appl
44	37	43.5	162	2	US-08-606-143-44	Sequence 44, Appl
45	37	43.5	811	1	US-08-480-604A-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-08-606-143-24
; Sequence 24, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-24

Query Match 100.0%; Score 85; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. NO. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DPLRNEYFFDRNRPS 15
Db 39 DPLRNEYFFDRNRPS 53
```

```
RESULT 2
US-08-606-143-26
; Sequence 26, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, MIN
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-606-143-26
;
; Query Match 100.0%; Score 85; DB 2; Length 150;
; Best Local Similarity 100.0%; Pred. NO. 1.5e-07;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DPLRNEYFFDRRPS 15
; Db 39 DPLRNEYFFDRRPS 53
;
; RESULT 3
; US-08-606-143-29
; Sequence 29, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, MIN
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
;
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-606-143-29
;
; Query Match 100.0%; Score 85; DB 2; Length 150;
; Best Local Similarity 100.0%; Pred. NO. 1.5e-07;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 DPLRNEYFFDRRPS 15
; Db 39 DPLRNEYFFDRRPS 53
;
; RESULT 4
; US-08-606-143-19
; Sequence 19, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, MIN
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; TITLE OF INVENTION: COMPOUNDS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
```

STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-19

Query Match 100.0%; Score 85; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 39 DPLRNEYFFDRNRPS 53

RESULT 5
US-08-606-143-4
; Sequence 4, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-4

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 39 DPLRNEYFFDRNRPS 53

RESULT 6
US-08-606-143-5
; Sequence 5, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:

APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-5

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRNRPS 15
|||||
DB 39 DPLRNEYFFDRNRPS 53

RESULT 7
US-08-606-143-6
; Sequence 6, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996

```
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-6

Query Match      100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRRPS 15
DB 39 DPLRNEYFFDRRPS 53

RESULT 8
US-08-606-143-7
Sequence 7, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-7

Query Match      100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRRPS 15
DB 39 DPLRNEYFFDRRPS 53

RESULT 9
US-08-606-143-9
Sequence 9, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-9

Query Match      100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRRPS 15
DB 39 DPLRNEYFFDRRPS 53

RESULT 10
US-08-606-143-10
Sequence 10, Application US/08606143
Patent No. 5856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
```

STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-10

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
|||||
DB 39 DPLRNEYFFDRNRPS 53

RESULT 11
US-08-606-143-12
Sequence 12, Application US/08606143
Patent No. 3856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600

TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-12

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
|||||
DB 39 DPLRNEYFFDRNRPS 53

RESULT 12
US-08-606-143-13
Sequence 13, Application US/08606143
Patent No. 3856155
GENERAL INFORMATION:
APPLICANT: Li, Min
TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,143
FILING DATE: 23-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 71756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEX: 25-3533
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-606-143-13

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DPLRNEYFFDRNRPS 15
|||||
DB 39 DPLRNEYFFDRNRPS 53

RESULT 13
US-08-606-143-15
; Sequence 15, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ. ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-15

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
|||||
DB 39 DPLRNEYFDRNRPS 53

RESULT 14
US-08-606-143-16
; Sequence 16, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ. ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-606-143-16

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPLRNEYFDRNRPS 15
|||||
DB 39 DPLRNEYFDRNRPS 53

RESULT 15
US-08-606-143-18
; Sequence 18, Application US/08606143
; Patent No. 5856155
; GENERAL INFORMATION:
; APPLICANT: LI, Min
; TITLE OF INVENTION: COMPOUNDS AND RELATED METHODS FOR
; TITLE OF INVENTION: MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Volt & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606,143
; FILING DATE: 23-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ. ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 152 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-606-143-18

Query Match 100.0%; Score 85; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DPLRNEYFFDRNRPS 15
|||
Db 39 DPLRNEYFFDRNRPS 53

Search completed: February 2, 2001, 10:36:29
Job time: 42 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:38:00 ; Search time 45.64 Seconds

(without alignments)
11.238 Million cell updates/sec

Title: US-09-273-217-2

Perfect score: 85

Sequence: 1 DPLRNEYFFDRNRPS 15

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq.36.*

- 1: /SIDSL/gcgdata/geneSeq/geneSeq/AA1980.DAT.*
- 2: /SIDSL/gcgdata/geneSeq/geneSeq/AA1981.DAT.*
- 3: /SIDSL/gcgdata/geneSeq/geneSeq/AA1982.DAT.*
- 4: /SIDSL/gcgdata/geneSeq/geneSeq/AA1983.DAT.*
- 5: /SIDSL/gcgdata/geneSeq/geneSeq/AA1984.DAT.*
- 6: /SIDSL/gcgdata/geneSeq/geneSeq/AA1985.DAT.*
- 7: /SIDSL/gcgdata/geneSeq/geneSeq/AA1986.DAT.*
- 8: /SIDSL/gcgdata/geneSeq/geneSeq/AA1987.DAT.*
- 9: /SIDSL/gcgdata/geneSeq/geneSeq/AA1988.DAT.*
- 10: /SIDSL/gcgdata/geneSeq/geneSeq/AA1989.DAT.*
- 11: /SIDSL/gcgdata/geneSeq/geneSeq/AA1990.DAT.*
- 12: /SIDSL/gcgdata/geneSeq/geneSeq/AA1991.DAT.*
- 13: /SIDSL/gcgdata/geneSeq/geneSeq/AA1992.DAT.*
- 14: /SIDSL/gcgdata/geneSeq/geneSeq/AA1993.DAT.*
- 15: /SIDSL/gcgdata/geneSeq/geneSeq/AA1994.DAT.*
- 16: /SIDSL/gcgdata/geneSeq/geneSeq/AA1995.DAT.*
- 17: /SIDSL/gcgdata/geneSeq/geneSeq/AA1996.DAT.*
- 18: /SIDSL/gcgdata/geneSeq/geneSeq/AA1997.DAT.*
- 19: /SIDSL/gcgdata/geneSeq/geneSeq/AA1998.DAT.*
- 20: /SIDSL/gcgdata/geneSeq/geneSeq/AA1999.DAT.*
- 21: /SIDSL/gcgdata/geneSeq/geneSeq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	Y42763	Rat potassium chan
2	85	100.0	495	20	Human cation chann
3	80	94.1	20	Y32013	Drosophila melanog
4	58	68.2	532	16	Mouse Kv1.7 volta
5	57	67.1	556	20	Caenorhabditis ele
6	49	57.6	499	20	Human potassium ch
7	43	50.6	513	17	Human K+ channel 1
8	43	50.6	513	19	Putative mature po
9	42	49.4	858	20	Human cation chann
10	41	48.2	477	20	Human potassium ch
11	40	47.1	157	20	Human Kv6.2 protei
12	40	47.1	466	20	Human Kv6.2 protei

13	40	47.1	494	17	R90765
14	40	47.1	494	19	M42996
15	40	47.1	495	20	Y33766
16	39	45.9	491	21	Y70454
17	38.5	45.3	490	20	Y34121
18	38.5	45.3	491	21	Y53780
19	37.5	44.1	506	21	Y44564
20	37.5	44.1	506	21	Y44566
21	37.5	44.1	506	21	Y44567
22	37.5	44.1	506	21	Y44568
23	37	43.5	457	20	W87970
24	37	43.5	635	20	Y24321
25	37	43.5	663	20	Y24322
26	37	43.5	680	20	Y24320
27	37	43.5	811	17	R95014
28	37	43.5	812	17	R95017
29	37	43.5	841	20	Y24318
30	37	43.5	862	20	W87971
31	37	43.5	1477	16	R67691
32	37	43.5	1477	18	W10424
33	37	43.5	1477	20	Y06819
34	37	43.5	2710	17	R95016
35	37	43.5	2710	19	W68387
36	36	42.4	35	18	R77937
37	36	42.4	35	16	M46130
38	36	42.4	35	19	W53090
39	36	42.4	35	21	Y51735
40	36	42.4	35	21	Y80432
41	36	42.4	48	19	W79087
42	36	42.4	90	21	Y64651
43	36	42.4	214	20	Y13524
44	36	42.4	256	20	Y34125
45	36	42.4	257	21	Y70452

ALIGNMENTS

RESULT 1

Y42763 standard; peptide: 15 AA.

Y42763:

20-DEC-1999 (first entry)

Rat potassium channel Kv1.2 intracellular N-terminal peptide #2.

Ion channel; potassium channel; vestibule; inhibitor; antibody;

polycationic; antagonist; hypertension; cardiac ischaemia;

bronchial constriction; neurological diseases.

Synthetic.

Rattus sp.

W09948927-A1.

30-SEP-1999.

19-MAR-1999: 99WO-US06019.

25-MAR-1998: 98US-0079268.

(CORR) CORNELL RES FOUND INC.

Huang X:

WPI: 1999-601205/51.

Designing specific blockers that bind to the external vestibule region

of ion channels, potentially useful for treating e.g. hypertension -

Example 3; Page 13; 40pp; English.

XX This sequence represents a peptide (#2), derived from the intracellular
 CC N-terminus of the rat delayed rectifier potassium channel Kv1.2.
 CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
 CC generate polyclonal antibodies. These antibodies were used as a control
 CC in studies of potassium channel inhibition by antibodies raised against
 CC the extracellular vestibule-derived peptides #1 (Y42761), #3
 CC (Y42763) and #4 (Y42764). The vestibule portion of potassium
 CC channels is located on the extracellular portion of the channel protein,
 CC and generally comprises a loop between the S5 transmembrane domain and
 CC the pore forming region of the channel, or between the pore forming
 CC region and the S6 transmembrane domain. Antibodies generated against
 CC vestibule peptides act as potassium channel inhibitors by binding to the
 CC vestibule portion, physically blocking the pore, or otherwise inducing a
 CC conformational change in the channel. These potassium channel blockers
 CC are potential therapeutic agents for e.g., hypertension, cardiac
 CC ischaemia, bronchial constriction and neurological diseases. Such
 CC inhibitors are specific for particular types of ion channel, and
 CC are produced by rational design based on known nucleotide and amino acid
 CC sequences for ion channels.
 XQ
 XX Sequence 15 AA;

Query Match	100.0%	Score 85;	DB 20;	Length 15;
Best local Similarity	100.0%	Pred. No. 9.3e-09;		
Matches 15; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 DPLRNEYFEDRNRPS 15
        1111111111111111
Db      1 dplrneyffdrnrps 15

```

RESULT	2
Y32014	
ID	Y32014 standard; Protein; 495 AA

DT 05-JAN-2000 (first entry)

DE Human cation channel protein.

KM Cation channel protein; CCP; ion transport; arrhythmia;
KM diabetes mellitus; seizure; asthma; hypertension; therapy;
KM protein engineering; human.

OS Homo sapiens.

	Key	Location/Qualifiers
FH	Region	61.119
FT		/note="crystal region"
FT		

PN W09947923-A2

PD 23-SEP-1999.

PF 22-MAR-1999; 99WO-US06307

PR 20-MAR-1998; 98US-0045529

PR 02-APR-1998; 98US-0054347

PA (UYRQ) UNIV ROCKEFELLER.

PI Mackinnon R;

DR WPI; 1999-601131/51

PT Assays for screening compounds which interact with cation channel

PS Claim 21; Page 135-137; 165pp; English.

XX.

CC The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs
CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-12). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP *in vivo*, such as cardiac
CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic CCPs.

Query Match	100.0%;	Score 85;	DB 20;	Length 495;
Best Local Similarity	100.0%;	Pred. No. 4.2e-07;		
Matches 15; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY 1 DPLRNEYFFDRNRPS 15
Db 74 dplrneyffdrnrps 88
```

RESULT	3
Y32013	
ID	Y32013 standard; Protein; 616 AA

AC Y32013;

DT 05-JAN-2000 (first entry)

Drosophila melanogaster cation channel protein

KW Cation channel protein; CCP; ion transport; arrhythmia;
 KW diabetes mellitus; seizure; asthma; hypertension; therapy;
 KW protein engineering.

OS *Drosophila melanogaster*.

FH	key	Location/Qualifiers
FT	Region	61.119
FT		/note="crystal region"

PN WO9947923-A2

PD 23-SEP-1999.

PF 22-MAR-1999; 99WO-US06307

PR 20-MAR-1998; 98US-0045529

XX

XX

XX XX

X

PT proteins, useful for providing agents

PS Claim 21; Page 133-135; 165pp; English

CC The present sequence represents a *Drosophila melanogaster* cation

CC screening potential drugs or agents which interact with CCPS using

CC recombinant DNA technology, to mimic the physiological function and

CC given in Y32013-22). An example of a mutated prokaryotic CCP is

CC given in Y32013-22). An example of a mutated prokaryotic CCP is
 CC given in Y32024. The crystal region of the CCP may also be used in
 CC the assay. The drugs or agents obtained can be used to treat
 CC conditions related to the function of CCP in vivo, such as cardiac
 CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
 CC hypertension. The invention has overcome the physical limitations
 CC regarding the isolation and purification of eukaryotic CCPs.

XX Sequence 556 AA;

Query Match 67.1%; Score 57; DB 20; Length 556;
 Best Local Similarity 83.3%; Pred. No. 0.037;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRN 12
 ||| |||||
 Db 72 dplneyffdrn 83

RESULT 6
 Y34122
 ID Y34122 standard; Protein; 499 AA.

XX Y34122;
 XX 30-NOV-1999 (first entry)

XX Human potassium channel K+hov9.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KW cardiovascular disorder; CNS disorder; renal disorder.

XX Homo sapiens.

XX MO9943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99WO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076687.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX WPI; 1999-527591/44.

XX N-PSDB; 211900.

XX New nucleic acids encoding mammalian K+hov potassium channel
 PT proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome

XX Claim 3: Page 56-57; 112pp; English.

XX This sequence represents the human K+hov9 potassium channel.
 CC K+hov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate the channel activity.
 CC K+hov9 is a voltage gated potassium channel. The gene's
 CC chromosomal location is 8q23, determined via PCR chromosomal
 CC localisation using primers 211922 and 211923. K+hov cDNAs were
 CC isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple
 CC independent clones. Potassium channels have critical roles in various
 CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,

CC It is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+hov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+hov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+hov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.

XX Sequence 499 AA;

Query Match 57.6%; Score 49; DB 20; Length 499;
 Best Local Similarity 66.7%; Pred. No. 0.82;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRN 12
 ||| |||||
 Db 95 npvdneffdrn 106

RESULT 7
 R90764
 ID R90764 standard; Protein; 513 AA.

XX R90764;

XX 25-APR-1996 (first entry)

XX Human K+ channel 1 mature protein.

XX Potassium channel; K+ channel 1; K+ channel 2; agonist; antagonist;
 KW hypertension; cancer.

XX Homo sapiens.

XX MO9603415-A1.

XX 08-FEB-1996.

XX 28-JUL-1994; 94WO-US08449.

XX 28-JUL-1994; 94WO-US08449.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Adams MD, Li Y, White OR;

XX WPI; 1996-116983/12.

XX N-PSDB; T12461.

XX Human potassium channel 1 and 2 proteins - also their agonists and
 PT antagonists, useful to treat e.g. hypertension or cancer,
 PT respectively

XX Claim 15: Page 39-41; 63pp; English.

XX 2 cDNA sequences (T12461-62) isolated from a human brain cDNA
 CC library code for K+ channel 1 (R90764) and K+ channel 2 (R90765),
 CC respectively. The proteins may be obtained by expression of the
 CC cDNAs in e.g. insect Sf9 or mammal COS cells. They can be used
 CC to screen potential agonists useful for treating hypertension,
 CC epilepsy, stroke, asthma, Parkinson disease, schizophrenia,
 CC anxiety, depression and neurodegeneration, and antagonists useful
 CC to treat migraine, autoimmune disease, cancer and graft rejection,
 CC or to raise diagnostic antibodies.

XX Sequence 513 AA;

Query Match 50.6%; Score 43; DB 17; Length 513;

Best Local Similarity 87.5%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NEYFDRN 12
|:|||||
DB 113 neffdrn 120

RESULT 8

W42995 ID W42995 standard; Protein: 513 AA.

AC W42995;

DT 30-APR-1998 (first entry)

DE Putative mature potassium channel 1 protein.

KM Potassium channel 1 protein; K⁺ channel; cellular homeostasis;

XX agonist; antagonist.

OS Homo sapiens.

PN US5710019-A.

PD 20-JAN-1998.

PF 05-JUN-1995; 95US-0464340.

PR 05-JUN-1995; 95US-0464340.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Adams MD, Li Y, White OR;

DR WPI: 1998-109815/10.

DR N-PSDB; V04873.

PT Potassium channel polypeptides and their agonists - useful for
PT treating e.g. epilepsy, stroke, hypertension and asthma also for
PT antibody production

PS Claim 3; Fig 1A-C; 35pp; English.

CC The present sequence represents a putative mature potassium (K⁺) channel 1
CC protein. The cDNA sequence was isolated from a cDNA library derived
CC from brain tissue. It is structurally related to the K⁺ channel gene
CC family. K⁺ channels are involved in normal cellular homeostasis and are
CC associated with a variety of disease states and immune responses.
CC The proteins can be used to produce antibodies for use in screening
CC assays for agonists or antagonists of K⁺ channel proteins. Agonists of
CC the polypeptides can be used in methods for treating hypertension,
CC epilepsy, stroke, asthma, Parkinson's disease, schizophrenia, anxiety,
CC depression and neurodegeneration. Antagonists of the polypeptides are
CC used for treating migraine, autoimmune diseases, cancer and graft
CC rejection.

XX SQ Sequence 513 AA;

Query Match 50.6%; Score 43; DB 19; Length 513;
Best Local Similarity 87.5%; Pred. No. 9.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NEYFDRN 12
|:|||||
DB 113 neffdrn 120

RESULT 9

Y32015 ID Y32015 standard; Protein: 858 AA.

XX

AC Y32015;

DT 05-JAN-2000 (first entry)

DE Human cation channel protein.

KM Cation channel protein; CCP; ion transport; arrhythmia;

XX diabetes mellitus; seizure; asthma; hypertension; therapy;

XX protein engineering; human.

OS Homo sapiens.

PN W09947923-A2.

PD 23-SEP-1999.

PF 22-MAR-1999; 99WO-US06307.

PR 20-MAR-1998; 98US-0045529.

PR 02-APR-1998; 98US-0054347.

PA (UYRO) UNIV ROCKEFELLER.

PI Mackinnon R;

DR WPI: 1999-601131/51.

PT Assays for screening compounds which interact with cation channel
PT proteins, useful for providing agents for treatment of diseases -
PS Claim 21; Page 137-140; 165pp; English.

CC The present sequence represents a human cation channel protein
CC (CCP). The invention provides an assay for screening potential
CC drugs or agents which interact with CCPs using prokaryotic CCPs
CC (such as those given in Y32009-12) mutated, using recombinant DNA
CC technology, to mimic the physiological function and chemical
CC properties of a functional eukaryotic CCP (such as those given in
CC Y32013-22). An example of a mutated prokaryotic CCP is given in
CC Y32024. The crystal region of the CCP may also be used in the
CC assay. The drugs or agents obtained can be used to treat
CC conditions related to the function of CCP in vivo, such as cardiac
CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
CC hypertension. The invention has overcome the physical limitations
CC regarding the isolation and purification of eukaryotic CCPs.

XX SQ Sequence 858 AA;

Query Match 49.4%; Score 42; DB 20; Length 858;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 NEYFDRN 12
|:|||||
DB 81 neyffdrn 88

RESULT 10
Y34127 ID Y34127 standard; Protein: 477 AA.

AC Y34127;

DT 30-NOV-1999 (first entry)

DE Human potassium channel K+hnov11.

KM Potassium channel; ataxia; arrhythmia; epilepsy; Barter's syndrome;

KW cardiovascular disorder; CNS disorder; renal disorder.
 OS Homo sapiens.
 XX MO9943696-A1.
 PN
 XX 02-SEP-1999.
 PD
 XX 22-FEB-1999; 99WO-US03826.
 PF
 XX 19-JAN-1999; 99US-0116448.
 PR 25-FEB-1998; 98US-0076687.
 PR 07-AUG-1998; 98US-0095836.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;
 XX WPI; 1999-527591/44.
 DR N-PSDB; Z11905.
 XX
 PT New nucleic acids encoding mammalian K+Hnov potassium channel
 PT proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
 XX
 PS Claim 3; Page 71-72; 112pp; English.
 XX
 CC This sequence represents the human K+Hnov1 potassium channel.
 CC K+Hnov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel, or
 CC accessory subunits that act to modulate the channel activity. K+Hnov1 is
 CC a 6 transmembrane domain, voltage gated, delayed rectifier potassium
 CC channel. K+Hnov cDNAs were isolated by extension of expressed sequence
 CC tags (ESTs) which were related but not identical to known human potassium
 CC channels. Potential polymorphisms detected as sequence variants between
 CC multiple independent clones. Potassium channels have critical roles in
 CC various cell types and biochemical pathways. Defective potassium channels
 CC are known to cause four human diseases: episodic ataxia with myokymia;
 CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+Hnov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+Hnov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+Hnov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.
 CC
 XX
 SQ Sequence 477 AA;
 XX
 QY
 Query Match 48.2%; Score 41; DB 20; Length 477;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 XX
 Db 1 DPLRNEYFFDRN 12
 1::1::11111
 63 dvvqrefyfdn 74
 XX
 RESULT 11
 Y50343
 ID Y50343 standard; Protein; 157 AA.
 XX
 AC Y50343;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Human Kv6.2 protein fragment.
 XX

KW Kv6.2; potassium channel protein; Kv2.1; myocardium; hippocampus; stroke;
 KW propafenone; voltage-dependent potassium channel; therapy; treatment;
 KW class IC anti-arrhythmic; cardiovascular disease; nervous system disease;
 KW antihypertensive; cardioprotective; learning disorder; memory disorder;
 KW neurodegenerative disorder; epilepsy; ischemia; Parkinson's disease;
 KW Alzheimer's disease.
 OS Homo sapiens.
 XX
 PN DE19841413-CL.
 XX
 PD 23-SEP-1999.
 PD
 XX 06-AUG-1998; 98DE-1041413.
 PF
 XX 06-AUG-1998; 98DE-1041413.
 PR
 XX 06-AUG-1998; 98DE-1041413.
 PR
 XX (GENT-) FORSCHUNGSGESELLSCHAFT GENTION MBH.
 PA
 XX
 PI Netzer R, Pongs O;
 XX
 DR WPI; 1999-519712/44.
 DR N-PSDB; Z23805.
 XX
 PT New potassium channel protein, Kv6.2, used to screen for specific
 PT modulators, potentially useful e.g. as antiarrhythmic agents
 XX
 PS Disclosure; Page 20; 42pp; German.
 XX
 CC This invention describes a novel potassium channel protein (I) Kv6.2.
 CC This protein forms, with the protein Kv2.1, voltage-dependent potassium
 CC channels that are expressed preferentially in the myocardium and
 CC hippocampus and have high affinity for propafenone. The channels are used
 CC to identify specific modulators which are potentially useful as
 CC therapeutic agents, particularly as class IC anti-arrhythmics, but more
 CC generally agents for treating cardiovascular or nervous system diseases,
 CC e.g. antihypertensives or cardioprotectants, or for treating learning and
 CC memory disorders or neurodegenerative disorders such as epilepsy,
 CC ischemia, stroke, or Parkinson's or Alzheimer's diseases. Nucleic acid
 CC that encodes (I) is used for recombinant production of (I), particularly
 CC to generate cells for drug screening. (I) is also used to raise specific
 CC antibodies. This sequence represents a fragment of the human Kv6.2
 CC protein described in the method of the invention.
 CC
 XX
 SQ Sequence 157 AA;
 XX
 QY
 Query Match 47.1%; Score 40; DB 20; Length 157;
 Best Local Similarity 58.3%; Pred. No. 8.7;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 XX
 Db 1 DPLRNEYFFDRN 12
 1::1::11111
 63 dvvtrdeffdrs 74
 XX
 RESULT 12
 Y50341
 ID Y50341 standard; Protein; 466 AA.
 XX
 AC Y50341;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE Human Kv6.2 protein.
 XX
 KW Kv6.2; potassium channel protein; Kv2.1; myocardium; hippocampus; stroke;
 KW propafenone; voltage-dependent potassium channel; therapy; treatment;
 KW class IC anti-arrhythmic; cardiovascular disease; nervous system disease;
 KW antihypertensive; cardioprotective; learning disorder; memory disorder;
 KW neurodegenerative disorder; epilepsy; ischemia; Parkinson's disease;
 KW Alzheimer's disease.
 XX

OS	Homo sapiens.
XX	
PN	DEJ9841413-C1.
XX	
PD	23-SEP-1999.
XX	
PF	06-AUG-1998; 98DE-1041413.
XX	
PR	06-AUG-1998; 98DE-1041413.
XX	
PA	(GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH.
XX	
PI	Netzer R, Pongs O;
XX	
DR	WPI: 1999-519712/44.
XX	N-PSTDB: Z23803.
PT	New potassium channel protein, Kv6.2, used to screen for specific modulators, potentially useful e.g. as antiarrhythmic agents -
PS	Claim 1; Page 13-15; 42pp; German.
CC	This invention describes a novel potassium channel protein (I) Kv6.2.
CC	This protein forms, with the protein Kv2.1, voltage-dependent potassium channels that are expressed preferentially in the myocardium and hippocampus and have high affinity for propafenone. The channels are used to identify specific modulators which are potentially useful as therapeutic agents, particularly as class IC anti-arrhythmics, but more generally agents for treating cardiovascular or nervous system diseases, e.g. antihypertensives or cardioprotectants, or for treating learning and memory disorders or neurodegenerative disorders such as epilepsy, ischemia, stroke, or Parkinson's or Alzheimer's diseases. Nucleic acid that encodes (I) is used for recombinant production of (I), particularly to generate cells for drug screening. (I) is also used to raise specific antibodies. This sequence represents the human Kv6.2 protein described in the method of the invention.
SQ	Sequence 466 AA:
Query Match	47.1%; Score 40; DB 20; Length 466;
Best Local Similarity	58.3%; Pred. No. 28;
Matches 7; Conservative	3; Mismatches 2; Indels 0; Gaps 0
OY	1 DPLRNEYFDNRN 12 : : : : Db 63 dvrirdefidfrs 74
RESULT 13	:
ID R90765	R90765 standard; Protein; 494 AA.
XX	
AC	R90765:
XX	
DT	25-APR-1996 (first entry)
XX	
DE	Human K+ channel 2 mature protein.
XX	
KM	Potassium channel; K+ channel 1; K+ channel 2; agonist; antagonist; hypertension; cancer.
XX	
OS	Homo sapiens.
XX	
PN	WO9603415-A1.
XX	
PD	08-FEB-1996.
XX	
PF	28-JUL-1994; 94WO-US08449.
XX	
PR	28-JUL-1994; 94WO-US08449.
XX	
PA	(HDMA-) HUMAN GENOME SCI INC.

[illegible]

CC family. K+ channels are involved in normal cellular homeostasis and are
CC associated with a variety of disease states and immune responses.
CC The proteins can be used to produce antibodies for use in screening
CC assays for agonists or antagonists of K+ channel proteins. Agonists of
CC the polypeptides can be used in methods for treating hypertension,
CC epilepsy, stroke, asthma, Parkinson's disease, schizophrenia, anxiety,
CC depression and neurodegeneration. Antagonists of the polypeptides are
CC used for treating migraine, autoimmune diseases, cancer and graft
CC rejection.

SO Sequence 494 AA;

Query Match 47.1%; Score 40; DB 19; Length 494;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRN 12

Db 71 dpqkrefyfd 82

RESULT 15

ID Y33766 standard; Protein; 495 AA.

AC Y33766;

DT 09-NOV-1999 (first entry)

DE hkv5.1 human brain-specific potassium channel.

KM Potassium channel; brain; hkv1.5; epilepsy; Alzheimer's disease;

KW synaptic transmission; electrical excitability; anxiety;

KM schizophrenia; Parkinson's disease; mental retardation; asthma;

KW migraine; stroke; neuronal modulatory subunit.

XX Homo sapiens.

XX MO9941372-A1.

PD 19-AUG-1999.

PF 11-FEB-1999; 99WO-GB00423.

PR 17-FEB-1998; 98US-0074999.

PA (ZENE) ZENCA LTD.

PI Aiyar J, Logsdon NJ, Zhou J;

DR WPI; 1999-527368/44.

DR N-PSDB; 206652, 206653.

PT New polynucleotide encoding the potassium channel modulatory subunit
PT human hkv5.1, used to identify modulators used to treat, prevent or
PT diagnose e.g. epilepsy or Alzheimer's disease

PS Claim 1; Page 92-93; 110pp; English.

CC This sequence is the human brain specific potassium channel hkv5.1
CC polypeptide. hkv5.1 is a neuronal modulatory subunit involved in
CC regulating synaptic transmission and electrical excitability in the
CC brain. The hkv5.1 polypeptide can be used to identify modulators of its
CC activity; to raise specific antibodies and to purify effectors from
CC natural sources. Sequences antisense to hkv5.1 are useful for diagnosis,
CC treatment, study and prevention of diseases mediated by potassium channel
CC activity in the brain and associated with dysfunctional neurons. These
CC diseases are cognitive, behavioural, psychological, neurodegenerative or
CC developmental, e.g. anxiety, schizophrenia, Alzheimer's or Parkinson's
CC diseases, mental retardation, asthma, migraine, epilepsy and stroke.
CC Particular applications are treatment of epilepsy or Alzheimer's disease.
CC Antibodies against hkv5.1 are used as therapeutic modulators; for

CC diagnostic measurement of hkv5.1 levels and for purification of hkv5.1 by
CC affinity chromatography.

SO Sequence 495 AA;

Query Match 47.1%; Score 40; DB 20; Length 495;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPLRNEYFFDRN 12

Db 72 dpqkrefyfd 83

Search completed: February 2, 2001, 10:38:02
Job Time: 135 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:41:47 ; Search time 20.39 Seconds

(without alignments)
22.173 Million cell updates/sec

Title: US-09-273-217-3

Sequence: 1 GAOPNDPSASEH 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	79	100.0	511 1	CIKD_HUMAN
2	79	100.0	511 1	CIKD_MOUSE
3	79	100.0	585 1	CIKD_RAT
4	71	89.9	638 1	CIKE_RAT
5	47	59.5	354 1	CAHC_HUMAN
6	47	59.5	582 1	CIKG_HUMAN
7	47	59.5	625 1	CIKG_RAT
8	44	55.7	2327 1	CCAB_MOUSE
9	44	55.7	2336 1	CCAB_RAT
10	42	53.2	1435 1	Y194_HUMAN
11	39	49.4	716 1	DVL3_HUMAN
12	39	49.4	716 1	DVL3_MOUSE
13	39	49.4	1060 1	UAY_EMENT
14	39	49.4	1136 1	CABA_BACTI
15	39	49.4	2869 1	RBPL_PLAIV
16	38	48.1	386 1	PSD4_ARATH
17	38	48.1	513 1	PPT1_YEAS
18	38	48.1	602 1	EUL_MOUSE
19	38	48.1	603 1	BPRV_BACNO
20	38	48.1	727 1	CCT1_HORSE
21	38	48.1	757 1	CIKE_HUMAN
22	38	48.1	769 1	CIKE_MOUSE
23	38	48.1	798 1	HMPB_DROME
24	38	48.1	889 1	CIKE_RAT
25	38	48.1	1841 1	CC12_SCCHO
26	38	48.1	2052 1	YDOB_SCCHO
27	37	46.8	181 1	CEN_ANTMA
28	37	46.8	215 1	YCK1_YEAS
29	37	46.8	350 1	MTRE_VITBL
30	37	46.8	432 1	Y1S4_YEAS
31	37	46.8	469 1	GLNA_AOUAE
32	37	46.8	561 1	VAT7_SCCHO
33	37	46.8	793 1	CLPA_RHOBL

ALIGNMENTS

RESULT 1	CIKD_HUMAN	STANDARD:	PRT:	511 AA.
AC	P48547;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.1 (KV4) (NGK2).			
GN	KCNK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93194190; PubMed=8449507;			
RA	Ried T., Rudy B., de Miera E., Lau D., Ward D.C., Sen K.;			
RT	"Localization of a highly conserved human potassium channel gene			
RT	(NGK2-KV4, KCNC1) to chromosome 11p15.";			
RL	Genomics 15:405-411(1993).			
RN	[2]			
RP	SEQUENCE OF 244-475 FROM N.A.			
RX	MEDLINE=93016011; PubMed=1400413;			
RA	Grismer S., Ganshanti S., Dethlefs B., McPherson J.D.,			
RT	Wasmuth J.J., Gutman G.A., Cahalan M.D., Chandry K.G.;			
RT	"The Shaw-related potassium channel gene, Kv3.1, on human chromosome			
RL	11, encodes the type 1 K+ channel in T cells.";			
RL	J. Biol. Chem. 267:20971-20979(1992).			
CC	- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM			
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED			
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE			
CC	MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH			
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL			
CC	GRADIENT.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS			
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT			
CC	EVERY THIRD POSITION.			
CC	- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL			
CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR			
CC	COMPARTMENTS.			
CC	- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER			
CC	CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; S56770; AAB25764.1; -			P17393 hepatitis b
DR	EMBL; M96747; AAA59458.1; -			P31380 saccharomyc
DR	MIM; 176258; -			Q24167 dtrosophila
DR	INTERPRO: IPR000636; -			Q07157 homo sapien
DR	INTERPRO: IPR003091; -			P51572 homo sapien
				P09272 varicella-z
				090346 cyprinus ca
				Q92238 mus musculu
				P38142 saccharomyc
				P35974 measles vir
				P03422 measles vir
				P26033 measles vir

DR	PFAM: PF00520; Ion_trans. 1.
DR	PRINTS: PF00169; KCHANNEL.
KM	Ion_cycl channel: Multisubstrate: Ion transport; Voltage-gated channel.
KM	glycoproteinh; Multigene family.
FT	DOMAIN 1 180 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 191 209
FT	DOMAIN 210 247
FT	TRANSMEM 248 276
FT	DOMAIN 268 276 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 277 295
FT	DOMAIN 296 308
FT	TRANSMEM 309 331
FT	DOMAIN 332 344
FT	TRANSMEM 345 366
FT	DOMAIN 367 414
FT	TRANSMEM 415 436
FT	DOMAIN 437 511
FT	CARBOHYD 220 230
FT	CARBOHYD 229 250
QO	SEQUENCE 511 AA: 57942 MW; 10A93447BF120AAB CRC64;

Query Match	100.0%	Score 79	DB 1	length 511
Best Local Similarity	100.0%	Pred. No.	9.9e-06	
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY      1 GAQPNDPSASEHTH 14
          |||||
Db      370 GAQPNDPSASEHTH 383
```

RESULT	2	
CIKD_MOUSE		
ID	CIKD_MOUSE	STANDARD;
511		PRT;
AA		

DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE KCAAC-GATED POTASSIUM CHANNEL PROTEIN KV3.1 (KV4) (NGX2)
GN NCN01.

RT Primary structure and functional expression from cDNAs.
RA Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells.
RA Numa S.;
RX Yokoyama S., Imoto K., Kawamura T., Higashida H., Iwabe N., Miyata T.
RP MEDLINE=90092535; PubMed=2599109;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.

CC
CC -1-
CC FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC

CC SUBSEQUENT LOCATION. INTERNAL MEMBRANE PROTEIN.
CC
CC -1- ALTERNATIVE PRODUCTS. RV4 ARISES FROM ALTERNATIVE SPLICING OF A
CC TRANSCRIPT FROM A GENE THAT ALSO ENCODES RV3.1.
CC
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.

CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAM POTASSIUM CHANNEL SUBFAMILY.
CC

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

```
DR EMBL: Y07521; CAA6814.1; -  
DR PIR: S07095; S07095.  
DR MGD: MG1:96667; KCNC1.  
DR INTERPRO: IPR000636; -.  
DR INTERPRO: IPR003091; -.  
DR Pfam: PF00520; Ion_trans_1.  
DR PRINTS: PR00169; KCHANNEL.
```

KW	IONIC CHANNEL; Transmembrane Ion Transport; Voltage-gated Channel
RW	Glycoprotein; Multigene family; Alternative splicing
FT	DOMAIN 1 190
FT	TRANSMEM 191 209
FT	DOMAIN 210 247
FT	TRANSMEM 248 267
FT	DOMAIN 268 276
FT	TRANSMEM 277 295
FT	DOMAIN 296 308
FT	TRANSMEM 309 331
FT	DOMAIN 332 344
FT	TRANSMEM 345 366
FT	DOMAIN 367 414
FT	TRANSMEM 415 436
FT	DOMAIN 437 511
FT	CARBOHYD 220 220
FT	CARBOHYD 229 229
QO	SOURCE 511 AA: 57928 MW: 50693588F1J2OF37 CR664: N-LINKED (GLCNAC...) (POTENTIAL). N-LINKED (GLCNAC...) (POTENTIAL).

Query Match	100.0%	Score 79;	DB 1;	Length 511;
Best Local Similarity	100.0%	Pred. NO.	9.9e-06;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      1 GAQPNDPSASETH 14
Db      370 GAQPNDPSASETH 383
```

RESULT	3
CIRD_RAT	
ID	CIRD_RAT
AC	P25122:
DT	01-MAY-1992 (Rel. 22, Created)
DT	01-MAY-1992 (Rel. 22, Last sequence update)
DT	15-JUL-1998 (Rel. 36, Last annotation update)
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.1 (KV4) (NGR2) (RAM2)
NCNCT.	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]

SEQUENCE FROM N.A.
MEDLINE-91219486; PubMed-2023341;
RA Leneu C.J., Williams J.B., Marshall J., Ievitan E.S., Oliva C.,
RA Smith J.S., Attanavage J., Follander K., Stein R.B., Swanson R.,
RA Kaczmarek L.K., Bihrow S.A.,
RT "Alternative splicing contributes to K+ channel diversity in the
RT mammalian central nervous system.,"
NL Proc. Natl. Acad. Sci. U.S.A. 88:3932-3936(1991).
[2]

RT "Characterization of a Shaw-related potassium channel family in rat
RA Voh R., Pongs O.,
RA Becht S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,
RA Rettig J., Wunder F., Stocker M., Lichtinghagen R., Mastiaux F.,
RX MEDLINE=92331595; PubMed=1378332;
RP SEQUENCE FROM N.A.

EMBO J. 11:2473-2486(1992).
-1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE

MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: BRAIN.

-1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

-1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.

THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

EMBL: M68880; AAA41501.1; -
 EMBL: X62840; CAA4464.1; -
 DR PIR: A39395; A39395.
 DR PIR: S22704; S22704.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFAM: PF00520; ion.trans. 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW IONIC CHANNEL; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Alternative splicing.
 FT DOMAIN 1 190
 FT TRANSMEM 191 209
 FT DOMAIN 210 247
 FT TRANSMEM 248 267
 FT TRANSMEM 268 276
 FT TRANSMEM 277 295
 FT TRANSMEM 296 308
 FT TRANSMEM 309 331
 FT TRANSMEM 332 344
 FT TRANSMEM 345 366
 FT DOMAIN 367 414
 FT TRANSMEM 415 436
 FT DOMAIN 437 585
 FT CARBOHYD 220 229
 FT CARBOHYD 229 239
 FT VARSPPLIC 502 511
 FT VARSPPLIC 512 585
 FT VARSPPLIC 585 585
 FT SEQUENCE 585 AA; 65857 MW; DDAED32848E2DCF CRC64;

Query Match 100.0%; Score 79; DB 1; Length 585;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH14
 DB 370 GAOPNDPSASEH14 383

RESULT 4
 CITE_RAT STRAND: PRT: 638 AA.
 AC P22462; P22461; P22463; Q63735;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.2 (KSHITTA).
 GN KCNC2.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS KV3.2B AND KV3.2C).
 RC TISSUE-BRAIN:
 RX MEDLINE-91348257; PubMed-1879548;
 RA Luneau C.J., Wiedmann R., Smith J.S., Williams J.B.;
 RT "Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.";
 RL FEBS Lett. 288:163-167(1991).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM KV3.2B).
 RX MEDLINE-92262488; PubMed-1374908;
 RA Baker H., Pollock J., Ellisman M., Kentros C., Miera E., Serodio P.,
 RT Weiser M., Rudy B., Fuhlring D.;
 RL "Region-specific expression of a K⁺ channel gene in brain.";
 RN Proc. Natl. Acad. Sci. U.S.A. 89:4603-4607(1992).
 RP [3]
 RP SEQUENCE FROM N.A. (ISOFORM KSHITTA.1).
 RC TISSUE-BRAIN:
 RX MEDLINE-90311375; PubMed-2367536;
 RA McCormack T., de Miera E.C.V.-S., Rudy B.;
 RT "Molecular cloning of a member of a third class of Shaker-family K⁺ channel genes in mammals.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5227-5231(1990).
 RN [4]
 RP REVISIONS.
 RX MEDLINE-91219512; PubMed-2023956;
 RA McCormack T., de Miera E.C.V.-S., Rudy B.;
 RT "Molecular cloning of a member of a third class of Shaker-family K⁺ channel genes in mammals.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:4060-4060(1991).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM GT10).
 RX MEDLINE-92331599; PubMed-1378392;
 RA Rettig J., Wunder F., Stocker M., Lichtinghagen R., Mastiaux F.,
 RT Beckh S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,
 RL Voh R., Pongs O.;
 RL "Characterization of a Shaw-related potassium channel family in rat brain.";
 RL EMBO J. 11:2473-2486(1992).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF KV3.2 ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

EMBL: M59211; AAA41819.1; -
 DR EMBL: M59313; AAA41820.1; ALT_SEQ.
 DR EMBL: M84203; AAA42143.1; -
 DR EMBL: M34052; AAA42142.1; -
 DR EMBL: X62839; CAA44643.1; -

Query Match	Best Local Similarity	89.9%	Score 71:	DB 1:	Length 638:
Matches 13: Conservative	100.0%	Pred. No. 0.00026:			
	0:	Mismatches 0:	Indels 0:	Gaps 0:	
0y 1 GAOPNDPSASERT 13					
Db 407 GAOPNDPSASERT 419					
RESULT 5					
CAHC_HUMAN	STANDARD:	PRT:	354 AA.		
AC 043570:					
DT 15-JUL-1999 (Rel. 38, Created)					
DT 15-JUL-1999 (Rel. 38, Last sequence update)					
DT 15-JUL-1999 (Rel. 38, Last annotation update)					
DE CARBONIC ANHYDRASE XII PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE XII) (CA-XII) (TUMOR ANTIGEN HOM-RCC-3.1.3).					
DE CA12.					
GN					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
RN [1]					
RP SEQUENCE FROM N.A.					
RA MEDLINE=98301622; PubMed=9636197;					
RA Tureci O., Sahin U., Vollmar E., Siemer S., Gottert E., Seltz G.,					
RA Turekli A.K., Shah G.N., Grubb J.H., Pfrendershub M., Sly W.S.:					
RT "Human carbonic anhydrase XII: cDNA cloning, expression, and					
RT chromosomal localization of a carbonic anhydrase gene that is					
RT overexpressed in some renal cell cancers."					
RL Proc. Natl. Acad. Sci. U.S.A. 95:7608-7613(1998).					
RP (2)					
RP SEQUENCE FROM N.A.					
RA MEDLINE=98445416; PubMed=9770531;					
RA Ivanov S.V., Kuzmin I., Wei M.-H., Pack S., Geil L., Johnson B.E.,					
RA Stanbridge E.J., Lerman M.I.;					

RT	"down-regulation of transmembrane carbonic anhydrase in renal cell carcinoma cell lines by wild-type von Hippel-Lindau transgenes."
RL	Proc. Natl. Acad. Sci. U.S.A. 95:12596-12601(1998).
CC	-1- FUNCTION: REVERSIBLE HYDRATATION OF CARBON DIOXIDE.
CC	-1- CATALYTIC ACTIVITY: H(2)CO(3) + CO(2) + H(2)O.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COLON, KIDNEY, AND PROSTATE AND MODERATELY EXPRESSED IN PANCREAS, OVARY, AND TESTIS.
CC	-1- SIMILARITY: BELONGS TO THE EUKARYOTIC-TYPE CARBONIC ANHYDRASE FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or_send_an_email_to_license@isb-slb.ch).
CC	-----
DR	EMBL; AF051882; AAC39789.1; -
DR	EMBL; AF037335; AAC63952.1; -
DR	MIM; 603263; -
DR	INTERPRO: IPR001148; -
DR	PFAM: PF00194; carb.anhydrase: 1.
DR	PROSITE, PS00162; EUC_CO2_ANHYDRASE; 1.
KW	Lysase; Zinc; Transmembrane; Signal.
FT	SIGNAL 1 24 POTENTIAL.
FT	CHAIN 25 354 CARBONIC ANHYDRASE XII.
FT	DOMAIN 25 301 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 302 322 POTENTIAL.
FT	DOMAIN 323 354 CYTOPLASMIC (POTENTIAL).
FT	METAL 119 119 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL 121 121 ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL 145 145 ZINC (CATALYTIC) (BY SIMILARITY).
FT	CARBOHYD 28 28 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD 80 80 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD 162 162 N-LINKED (GLCNAc. . .) (POTENTIAL).
SO	SEQUENCE 354 AA; 39451 MW; 901621BF2CA6C0C CRC64;
QY	4 PNDPSASEPT 13
Db	125 PNDPSASEPT 134
RESULT 6	
CIRK_HUMAN	
ID CIRK_HUMAN	STANDARD; PRT: 582 AA.
AC C03721;	
DT 15-JUL-1998	(Rel. 36, Created)
DT 15-JUL-1998	(Rel. 36, Last sequence update)
DT 15-JUL-1998	(Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.4 (KSHIITIC).	
GN KCNC4.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
PN (1)	
RP SEQUENCE FROM N.A.	
RC TISSUE-BRAIN:	
RX MEDLINE-92396711; PubMed-1381835;	
RA Vega-Saenz de Miera E., Moreno H., Fruhling D., Kentros C., Rudy B.;	
RT "Cloning of Shit1 (Shaw-like) cDNAs encoding a novel high-voltage-	
RT activating, TEA-sensitive, type-A K+ channel."	
RL Proc. R. Soc. Lond., B. Biol. Sci. 248:9-18(1992).	
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH	

CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M64676; AA57263.1; -.
 DR HSSP: Q63734; 1ZTN.
 DR MIM: 176265; -.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR003091; -.
 DR PFAM: PF00520; Ion.trans. 1.
 DR PRINTS: PR00169; KCHANNEL.
 KM Glycoprotein; Transmembrane; Ion transport; Voltage-gated channel;
 KM Ionic channel; Multigene family; Phosphorylation.
 FT DOMAIN 1 226
 FT TRANSMEM 227 247
 FT DOMAIN 248 277
 FT TRANSMEM 278 298
 FT DOMAIN 299 312
 FT TRANSMEM 313 333
 FT DOMAIN 334 380
 FT TRANSMEM 381 401
 FT DOMAIN 402 422
 FT TRANSMEM 423 443
 FT DOMAIN 444 451
 FT TRANSMEM 452 472
 FT DOMAIN 473 582
 FT CAROHD 256 256
 FT CAROHD 265 265
 SQ SEQUENCE 582 AA: 64527 MW: 85855A4CA3A9F CRC64;

Query Match 59.5%; Score 47; DB 1; Length 582;
 Best Local Similarity 53.8%; Pred. No. 2.1;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13
 DB 406 GARSPDPRGNDHT 418
 11:11 :11

RESULT 7
 CING_RAT STANDARD: PRT; 625 AA.
 AC 063734;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.4 (RAM3).
 GN KCNC4.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92331599; PubMed=1378392;
 RA Reting J., Wunder F., Stocker M., Lichtinghagen R., Mastiaux F.,
 RA Bech S., Kues W., Pedarzani P., Schroeter K.H., Ruppersberg J.P.,

RA Voh R., Pongs O.;
 RT "Characterization of a Shaw-related potassium channel family in rat
 RT brain.";
 RL EMBL J. 11:2473-2486(1992).
 RN [2]
 RP STRUCTURE BY NMR OF 1-30.
 RX MEDLINE=97152495; PubMed=9000078;
 RA Antz C., Geyer M., Fakler B., Scholt M.K., Guy H.R., Frank R.,
 RA Ruppersberg J.P., Kalblitzer H.R.;
 RT "NMR structure of inactivation gates from mammalian voltage-dependent
 RT potassium channels";
 RL Nature 385:272-275(1997).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAW POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X62841; CAA44645.1; -.
 DR PDB: 1ZTN; 05-JUN-97.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR003091; -.
 DR PFAM: PF00520; Ion.trans. 1.
 DR PRINTS: PR00169; KCHANNEL.
 KM Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation; 3D-structure.
 SQ SEQUENCE 625 AA: 68435 MW: C3A86BC8231FB04 CRC64;

Query Match 59.5%; Score 47; DB 1; Length 625;
 Best Local Similarity 53.8%; Pred. No. 2.3;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13
 DB 407 GARSPDPRGNDHT 419
 11:11 :11

RESULT 8
 CCAB_MOUSE STANDARD: PRT; 2327 AA.
 AC 055017; Q60609;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM
 DE CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL
 DE III) (BIII).
 GN CACNA1B OR CACNA1A5 OR CCHN1A OR CACHS5.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL; TISSUE=BRAIN;

RA	Hong T.Birnbaumer L.:
RT	"Nucleotide sequence polymorphism of mouse alpha B."
RL	Submitted (Jan-1998) to the EMBL/genbank/dbdb databases.
RN	(2)
RP	SEQUENCE FROM N.A. (ISOFORMS NB1 AND NB2).
RC	TISSUE-NEUROBLASTOMA:
RX	MEDLINE=94139684; PubMed=8307146;
RA	Coppola T., Waldmann R., Borsetto M., Heurteaux C., Romey G.,
RT	Mattel M.-G., Lazdunski M.:
RT	Molecular cloning of a murine N-type calcium channel alpha 1 subunit.
RT	Evidence for isoforms, brain distribution, and chromosomal
RT	localization ";
RL	FEBS lett. 338:1-5(1994).
-I-	FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE
CC	ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC	IN A VARIETY OF CALCIUM DEPENDENT PROCESSES, INCLUDING MUSCLE
CC	CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC	CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B
CC	GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS
CC	BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED
CC	BY OMEGA-CONOTOXIN-GVIA (OMEGA-CYX-GVIA) AND BY OMEGA-AKATOXIN-
CC	IIVA (OMEGA-AGA-IITA). THEY ARE HOWEVER INSENSITIVE TO
CC	DIHYDROPYRIDINES (DHP), AND OMEGA-AKATOXIN-IVA (OMEGA-AGA-IVA).
CC	CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN
CC	DIRECTED MIGRATION OF IMMATURE NEURONS.
-I-	SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC	COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC	IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC	FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC	SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC	CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DDELTA
CC	LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; NB1 (SHOWN HERE) AND NB2; ARE
CC	PRODUCED BY ALTERNATIVE SPLICING.
-I-	TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN.
CC	HIGHEST LEVELS IN PYRAMIDAL CELL LAYERS C1, C2 AND C3 OF THE
CC	HIPPOCAMPLUS, IN THE DENTATE GYRUS, IN THE CORTEX LAYERS 2 ET 4, IN
CC	THE SUBICULUM AND THE HABENULA.
-I-	DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC	HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC	POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC	PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC	SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
-I-	PMA: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND GSKP
CC	(BY SIMILARITY).
-I-	SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC	FAMILY.
-I-	CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 1924
CC	TO 1934 AND 2121 TO 2127 DUE TO FRAMESHIFTS.

CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@sib-stb.ch).

DR	EMBL: AF042317; AAB97840.1; -
DR	EMBL: U04959; AAB60437.1; ALT_FRAME.
DR	MGI: MGI:88296; CACNA1B.
DR	INTERPRO: IPR000636; -
DR	INTERPRO: IPR002077; -
DR	PFAM: PF00520; Ion_trans_4.
DR	PRINTS: PR00167; CACHANNEL.
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW	Calcium channel; Glycoprotein; Repeat; Multigene family;
KW	Calcium-binding; Phosphorylation; AMP-binding; Alternative splicing;
KW	Polymorphism.
FT	REPEAT 82 359 I.
FT	REPEAT 468 712 II.
FT	REPEAT 1126 1412 III.


```

FT DOMAIN 357 483 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 484 503 S1 OF REPEAT II (POTENTIAL).
FT DOMAIN 504 517 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 518 537 S2 OF REPEAT II (POTENTIAL).
FT DOMAIN 538 545 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 546 564 S3 OF REPEAT II (POTENTIAL).
FT DOMAIN 565 575 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 576 593 S4 OF REPEAT II (POTENTIAL).
FT DOMAIN 594 612 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 613 632 S5 OF REPEAT II (POTENTIAL).
FT DOMAIN 633 685 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 686 710 S6 OF REPEAT II (POTENTIAL).
FT DOMAIN 711 1143 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1144 1167 S1 OF REPEAT III (POTENTIAL).
FT DOMAIN 1168 1184 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1185 1204 S2 OF REPEAT III (POTENTIAL).
FT DOMAIN 1205 1212 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1213 1235 S3 OF REPEAT III (POTENTIAL).
FT DOMAIN 1236 1250 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1251 1265 S4 OF REPEAT III (POTENTIAL).
FT DOMAIN 1266 1286 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1287 1306 S5 OF REPEAT III (POTENTIAL).
FT DOMAIN 1307 1392 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1393 1417 S6 OF REPEAT III (POTENTIAL).
FT DOMAIN 1418 1474 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1475 1493 S1 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1494 1507 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1508 1527 S2 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1528 1536 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1537 1555 S3 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1556 1563 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1564 1582 S4 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1583 1601 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 1602 1621 S5 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1622 1683 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 1684 1703 S6 OF REPEAT IV (POTENTIAL).
FT DOMAIN 1704 2336 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 2049 2053 POLY-HIS.
FT DOMAIN 2115 2119 BINDING TO THE BETA SUBUNIT.
FT TRANSSEM 379 396 ATP (POTENTIAL).
FT DOMAIN 452 459 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT TRANSSEM 314 314 (BY SIMILARITY).
FT SITE 664 664 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT TRANSSEM 1367 1367 (BY SIMILARITY).
FT SITE 1655 1655 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT TRANSSEM 1719 1719 CALCIUM ION SELECTIVITY AND PERMEABILITY
FT CA_BIND 1737 1748 (BY SIMILARITY).
FT CARBOHYD 256 256 PHOSPHORYLATION (BY CARB) (POTENTIAL).
FT CARBOHYD 1563 1563 BY SIMILARITY.
FT CARBOHYD 1675 1675 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1538 1538 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 1579 1579 N -> D (IN REF. 2).
FT CONFLICT 1579 1579 C -> L (IN REF. 2).
SQ SEQUENCE 2336 AA; 262254 MW; 8D50AF67834FD1BC CRC64;

```

```

Query Match 55.7%; Score 44; DB 1; Length 2336;
Best Local Similarity 58.3%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 GAQPNPDSASEH 12
Db 1066 GSPSPDSSTVH 1077

```

```

RESULT 10
Y194_HUMAN STANDARD; PRT; 1435 AA.
AC 012766;
DT 01-NOV-1997 (Rel. 35, Created)

```

```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN KIAA0194 (PRAGMENT).
GN KIAA0194.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW.
RX MEDLINE=96281124; PubMed=8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V.
RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 3:17-24(1996).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D83778; BAA12107.1; -.
DR INTERPRO; IPR000910; -.
DR PFM; PFM0505; HMG-box 1.
KW Hypothetical protein.
FT NO_TER 1
SQ SEQUENCE 1435 AA; 156908 MW; 40469202E81F07A CRC64;

```

```

Query Match 53.2%; Score 42; DB 1; Length 1435;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

```

```

OY 1 GAQPN--DPSASEHT 13
Db 1319 GLQPNPGDPSAGHHS 1333

```

```

RESULT 11
DVL3_HUMAN STANDARD; PRT; 716 AA.
AC 092997; 092607; 014642; 013531;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE SEGMENT POLARITY PROTEIN DISHEVELLED DVL-3 (DISHEVELLED-3)
DE (DSH HOMOLOG 3) (KIAA0208).
GN DVL3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN.
RX MEDLINE=98008870; PubMed=9344861;
RA Bul T.D., Beier D.R., Jonssen M., Smith K., Dorrington S.M.,
RA Kellman L., Kearney L., Regan R., Sussman D.D., Harris A.L.;
RT "cDNA Cloning of a human dishevelled DVL-3 gene, mapping to 3q27, and
RT expression in human breast and colon carcinomas."
RL Biochem. Biophys. Res. Commun. 239:510-516(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97336056; PubMed=9192851;
RA Semenov M.V., Snyder M.;
RT "Human dishevelled genes constitute a DHR-containing multigene
RL family."
RL Genomics 42:302-310(1997).
RN [3]
RP SEQUENCE FROM N.A.

```

```
RC TISSUE-BRAIN;
RX MEDLINE-96414301; PubMed-8817329;
RA Pizzuti A., Amati F., Calabrese G., Mari A., Colosimo A., Silani V.,
RA Gardino L., Ratti A., Penso D., Calza L., Palka G., Scariato G.,
RA Novelli G., Dallapiccola B.;
RT "cDNA characterization and chromosomal mapping of two human homologues
RT of the prosopha dishevelled polarity gene.";
RL Hum. Mol. Genet. 5:953-958(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW;
RX MEDLINE-97191544; PubMed-9039502;
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. VI.
RT The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by
RT analysis of cDNA clones from cell line KG-1 and brain.";
RL DNA Res. 3:321-329(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
CC
CC -1- MEDIATED BY MULTIPLE WNT GENES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U75651; AAB84228.1; -
DR EMBL: AF006013; AAB65244.1; -
DR EMBL: U49262; AAB47447.1; -
DR EMBL: D86963; BAA13199.1; -
DR HSSP: P31016; 1BFE.
DR MIM: 601368; -
DR INTERPRO: IPR000591; -
DR INTERPRO: IPR001158; -
DR INTERPRO: IPR001478; -
DR PFAM: PF00610; DEP; 1.
DR PFAM: PF00778; DIX; 1.
DR PFAM: PF00595; PDZ; 1.
DR Developmental protein.
KW DOMAIN
FT 249 336
FT CONFLICT 2 2 DHR.
FT CONFLICT 76 76 G->D (IN REF. 3).
FT CONFLICT 102 102 S->Y (IN REF. 1).
FT CONFLICT 151 151 P->S (IN REF. 3).
FT CONFLICT 182 182 G->W (IN REF. 3).
FT CONFLICT 182 182 S->N (IN REF. 3).
FT CONFLICT 218 218 K->N (IN REF. 3).
FT CONFLICT 222 222 R->W (IN REF. 3).
FT CONFLICT 230 230 E->D (IN REF. 3).
FT CONFLICT 233 233 S->C (IN REF. 3).
FT CONFLICT 236 236 S->T (IN REF. 3).
FT CONFLICT 239 239 T->S (IN REF. 3).
FT CONFLICT 242 242 T->A (IN REF. 3).
FT CONFLICT 303 303 N->K (IN REF. 3).
FT CONFLICT 431 431 R->C (IN REF. 3).
FT CONFLICT 450 450 W->C (IN REF. 3).
FT CONFLICT 465 465 R->P (IN REF. 3).
FT CONFLICT 472 472 L->V (IN REF. 3).
FT CONFLICT 543 543 P->R (IN REF. 3).
FT CONFLICT 554 554 FP->LG (IN REF. 2).
FT CONFLICT 629 629 A->T (IN REF. 3).
FT CONFLICT 633 633 S->I (IN REF. 3).
FT CONFLICT 682 716 PRGRDLASVPELTASRQSPFMANGNSEFFVDVA -> LK
FT SEQUENCE 716 AA; 78054 MM; BIA55EBF9507D06E CRC64;
SQ
```

```
Best Local Similarity 46.2%; Pred. No. 56;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AQPNDPSASERTH 14
Db 622 SERSGPASERSH 634
RESULT 12
DVL3_MOUSE STANDARD; PRT; 716 AA.
AC 061062;
DT 30-MAY-2000 (Rel. 39, Last Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-3 (DISHEVELLED-3)
DE (DSH HOMOLOG 3).
GN DVL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-BRAIN;
RX MEDLINE-97081279; PubMed-8922524;
RA Tseng M., LiJam N., Yang Y., Belier D.R., Wynshaw-Boris A.,
RA Sussman D.J.;
RT "Isolation and characterization of mouse dishevelled-3.";
RL Dev. Dyn. 207:253-262(1996).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
CC
CC -1- MEDIATED BY MULTIPLE WNT GENES.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: CONTAINS 1 PDZ/DRH DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U41285; AAB01761.1; -
DR HSSP: P31016; 1BFE.
DR MGD: MGI:108100; DVL3.
DR INTERPRO: IPR000591; -
DR INTERPRO: IPR001158; -
DR INTERPRO: IPR001478; -
DR PFAM: PF00610; DEP; 1.
DR PFAM: PF00778; DIX; 1.
DR PFAM: PF00595; PDZ; 1.
DR Developmental protein.
KW DOMAIN
FT 249 336
FT SEQUENCE 716 AA; 78122 MM; 35412C03202301P0 CRC64;
SQ
```

Query Match 49.4%; Score 39; DB 1; Length 716;

Query Match 49.4%; Score 39; DB 1; Length 716;

Best Local Similarity 46.2%; Pred. No. 56;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 AQPNDPSASERTH 14
Db 622 SERSGPASERSH 634
RESULT 13
DVL3_MOUSE STANDARD; PRT; 1060 AA.
AC P49413;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

DB 2695 NDPQSETH 2704

Search completed: February 2, 2001, 10:41:50
Job time: 314 sec

```
FT CONFLICT 496 496 K -> R (IN REF. 4).
FT CONFLICT 519 519 G -> GG (IN REF. 4).
FT CONFLICT 551 572 LNVSVLOGVSRGTTISTESTF -> IECDHMYKEPLEEQ
FT CONFLICT 594 594 RLQONYV (IN REF. 4).
FT CONFLICT 687 690 F -> N (IN REF. 4).
FT CONFLICT 721 721 ELYP -> GIIS (IN REF. 4).
FT CONFLICT 823 832 A -> R (IN REF. 4).
FT CONFLICT 836 837 SNRCETSAVP -> LIVSVRCA (IN REF. 4).
FT CONFLICT 902 902 GN -> WD (IN REF. 4).
FT CONFLICT 1015 1015 E -> R (IN REF. 4).
FT CONFLICT 1015 1015 G -> V (IN REF. 4).
SQ SEQUENCE 1136 AA; 127764 MW; 8AC4EC26FE3E9B5 CRC64;
```

Query Match 49.4%; Score 39; DB 1; Length 1136;
Best Local Similarity 45.5%; Pred. No. 93;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 NDPQSETH 14
|||: |||: |||
DB 433 PNOPTVNDTH 443

```
RESULT 15
RBP1_PLAVB
ID RBP1_PLAVB STANDARD: PRT: 2869 AA.
AC 000798.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE RETICULOCYTE BINDING PROTEIN 1 PRECURSOR.
GN RBP1.
OS Plasmodium vivax (strain Belen).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN {}
RP SEQUENCE FROM N.A.
RX MEDLINE=92315338; PubMed=1617731;
RA Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
RT "A reticulocyte-binding protein complex of Plasmodium vivax
merozoites."
RL Cell 69:1213-1226(1992).
CC -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO
HUMAN RETICULOCYTE CELLS.
CC -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M88097; AAA29743.1; -.
DR HSSP: P36956; IAM9.
KW Malaria; Receptor; Signal; Transmembrane.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 2869 RETICULOCYTE BINDING PROTEIN 1.
FT DOMAIN 18 2807 EXTRACELLULAR.
FT TRANSMEM 2808 2826 POTENTIAL.
FT DOMAIN 2827 2869 CYTOPLASMIC.
FT SITE 1030 1032 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 2599 2601 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 2869 AA; 330213 MW; B9DBE44205EBCF CRC64;
```

Query Match 49.4%; Score 39; DB 1; Length 2869;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 NDPQSETH 14
|||: |||: |||

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:39:09 ; Search time 62.83 Seconds

(without alignments)
26.117 Million cell updates/sec

Title: US-09-273-217-3
Perfect score: 79
Sequence: 1 GAQPNPDSASEH14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	585	6 Q9XSJ8	Q9XSJ8 canis faml
2	70	88.6	587	13 Q9IA29	Q9IA29 oncorhynch
3	59	74.7	279	13 Q9IA28	Q9IA28 oncorhynch
4	52	65.8	273	2 Q9ZBS9	Q9ZBS9 streptomyc
5	47	59.5	325	10 O65152	O65152 malus domes
6	45	57.0	180	5 Q9VW73	Q9VW73 drosophila
7	45	57.0	214	2 Q9RYV3	Q9RYV3 deinococcus
8	44	55.7	872	5 Q9VAMS	Q9VAMS drosophila
9	44	55.7	2333	11 Q89089	Q89089 ratius norv
10	42	53.2	378	4 Q9UMF4	Q9UMF4 homo sapien
11	42	53.2	592	13 Q9PVD1	Q9PVD1 xenopus lae
12	42	53.2	803	3 Q13657	Q13657 schizosacch
13	42	53.2	1932	3 Q06409	Q06409 saccharomyc
14	41	51.9	209	3 Q9P7C6	Q9P7C6 schizosacch
15	41	51.9	276	2 Q9X908	Q9X908 streptomyc
16	41	51.9	276	2 Q9ZVMS	Q9ZVMS streptomyc
17	41	51.9	325	10 Q9ZVMS	Q9ZVMS streptomyc
18	41	51.9	435	10 Q9XEU9	Q9XEU9 oryza sativ
19	40	50.6	615	11 Q9J398	Q9J398 mus musculu

20	40	50.6	757	6 Q9N015	Q9N015 macaca fasc
21	40	50.6	1711	5 Q96108	Q96108 plasmodium
22	40	50.6	6420	2 P95814	P95814 streptomyc
23	39	49.4	327	10 Q04391	Q04391 eucalyptus
24	39	49.4	339	2 Q96136	Q96136 salmoneilla
25	39	49.4	343	2 Q96026	Q96026 salmoneilla
26	39	49.4	348	2 Q96033	Q96033 salmoneilla
27	39	49.4	354	6 Q9WZ30	Q9WZ30 oryctolagus
28	39	49.4	457	4 Q13518	Q13518 homo sapien
29	39	49.4	508	12 Q95579	Q95579 bovine herp
30	39	49.4	548	4 Q9UG07	Q9UG07 homo sapien
31	39	49.4	603	2 Q96547	Q96547 bacteroides
32	39	49.4	683	5 Q09977	Q09977 ctenorhadi
33	39	49.4	701	5 Q24928	Q24928 elmeria ten
34	39	49.4	2656	5 Q9NE92	Q9NE92 leishmania
35	38	48.1	63	5 Q9VHW2	Q9VHW2 drosophila
36	38	48.1	114	12 Q86574	Q86574 human herpe
37	38	48.1	118	10 Q9XH41	Q9XH41 nicotiana t
38	38	48.1	177	10 P93003	P93003 arabidopsis
39	38	48.1	208	2 P95381	P95381 pseudomonas
40	38	48.1	222	2 P74298	P74298 synechocyst
41	38	48.1	286	3 Q9P5D1	Q9P5D1 neurospora
42	38	48.1	296	2 Q9RY19	Q9RY19 deinococcus
43	38	48.1	338	5 Q9VIR3	Q9VIR3 drosophila
44	38	48.1	350	5 Q21249	Q21249 ctenorhadi
45	38	48.1	373	13 Q92073	Q92073 g beta-1,4-

ALIGNMENTS

```

RESULT 1
ID Q9XSJ8 PRELIMINARY: PRT: 585 AA.
AC Q9XSJ8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-2000 (TREMBLrel. 14, Last annotation update)
DE GN KV3.1.
GN KV3.1.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ATRIUM;
RA Yue L., Mang Z., Rindt H., Nattel S.;
RT "Cloning and functional expression of cardiac Kv3.1 channels: A novel
RT molecular basis for cardiac delayed rectifier currents."
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF153198; AAD34618.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: PF00520; ion_trans; 1.
DR PIRAT: PR00169; KCHANNEL.
DR PRINTS: PR00169; KCHANNEL.
SQ SEQUENCE 585 AA; 65911 MW; 71A0805FAE64AAAE CRC64;

Query Match 100.0%; Score 79; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAQPNPDSASEH14
DB 370 GAQPNPDSASEH14 383

RESULT 2
Q9IA29 PRELIMINARY: PRT: 587 AA.
AC Q9IA29;

```

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE SHAW-RELATED POTASSIUM CHANNEL PROTEIN RAM1.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Panofen F., Rahe H., Stegmann J., Jeserich G.;
 RT "Molecular cloning and functional characterization of Shaw-related
 RL potassium channels of trout CNS."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF223409; AAF33249.1; -;
 KW Ionic channel.
 SQ SEQUENCE 587 AA; 66317 MW; A0CB46FA3CF17E86 CRC64;

Query Match 88.6%; Score 70; DB 13; Length 587;
 Best Local Similarity 85.7%; Pred. No. 0.00057;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHTH 14
 ||:|||||
 DB 357 GAOPNDPSASEHTH 370

RESULT 3
 OYIA28 PRELIMINARY; PRT; 279 AA.

AC O9IA28;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE SHAW-RELATED POTASSIUM CHANNEL PROTEIN RAM2 (FRAGMENT).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Panofen F., Rahe H., Stegmann J., Jeserich G.;
 RT "Molecular cloning and functional characterization of Shaw-related
 RL potassium channels of trout CNS."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF223410; AAF33250.1; -;
 KW Ionic channel.
 FT NON_TER 1
 FT NON_TER 279
 SQ SEQUENCE 279 AA; 31585 MW; 3483739F8B528B65 CRC64;

Query Match 74.7%; Score 59; DB 13; Length 279;
 Best Local Similarity 76.9%; Pred. No. 0.02;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13
 ||:|||||
 DB 253 GAOPNDPSASEHT 265

RESULT 4
 OY2BS9 PRELIMINARY; PRT; 273 AA.
 AC O92BS9;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE PUTATIVE GNTF FAMILY TRANSCRIPTIONAL REGULATOR.
 GN SCIA9.23.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Saunders D.C., Harris D.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RL the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 DR M01. Microbiol. 21:77-96(1996).
 DR EMBL; AL034446; CAA22393.1; -;
 DR INTERPRO; IPR000524; -;
 DR PFAM; PF00392; gntR; 1.
 SQ SEQUENCE 273 AA; 28699 MW; B82D49CD374B6F00 CRC64;

Query Match 65.8%; Score 52; DB 2; Length 273;
 Best Local Similarity 57.1%; Pred. No. 0.3;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHTH 14
 ||:|||||
 DB 43 GAEPDGPARGHEHTH 56

RESULT 5
 O65152 PRELIMINARY; PRT; 325 AA.
 AC O65152;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE PUTATIVE CINNAMYL ALCOHOL DEHYDROGENASE.
 GN CAD.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Rosales; Rosaceae; Malus.
 OX NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. FUJI;
 RA Lee J.-R., An G., Kim S.-R.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053084; AAC06319.1; -;
 DR MENDEL; 28908; Maldo; 2995; 28908.
 SQ SEQUENCE 325 AA; 35553 MW; 1AB7F5117ADA60CE CRC64;

Query Match 59.5%; Score 47; DB 10; Length 325;
 Best Local Similarity 63.6%; Pred. No. 2.5;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHTH 14
 ||||:||||
 DB 40 PNDPTKTEHLH 50

RESULT 6
 Q9VM73 PRELIMINARY; PRT; 180 AA.
 ID Q9VM73
 AC Q9VM73
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE CG14184 PROTEIN.
 GN CG14184.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RAmannatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iobagyan C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mottel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheelers F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 DR EMBL: AE003515; AAF9076.1;
 DR FLYBASE: FBgn0036932; CG14184.
 SQ SEQUENCE 180 AA; 20507 MW; 6BD11AA8107EECF4 CRC64;

AC Q9RYX3:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 22.6 KDA PROTEIN.
 GN DRA0170.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.S., Lam P., McDonald L., Utecherback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome Sequence of the Radioreistant Bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001862; AAF12308.1;
 DR TIGR: DRA0170;
 KW Hypothetical protein.
 SQ SEQUENCE 214 AA; 22623 MW; 387D762D007D8F35 CRC64;

Query Match 57.0%; Score 45; DB 2; Length 214;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEH 12
 |||||:|:|:|
 Db 129 GAOPQQAVERH 140

RESULT 8
 Q9VAM5 PRELIMINARY; PRT; 872 AA.
 ID Q9VAM5
 AC Q9VAM5
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE CG14514 PROTEIN.
 GN CG14514.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RAmannatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegum C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matzel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshireit A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003768; AAF56879.1; -;
 DR FLYBASE: FBgn0039654; CG14514.
 DR INTERPRO: IPR001487; -;
 DR PROSITE: PSS0014; BROMODOMAIN_2; 1;
 DR PROSITE: 872 AA; 94151 MW; 68EA3CF4749BCD0B CRC64;
 SO SEQUENCE

Query Match 55.7%; Score 44; DB 5; Length 872;
 Best Local Similarity 70.0%; Pred. No. 21;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PNDPSASEHT 13
 Db 713 PNDPSASEHT 722

RESULT 9
 ID 089089 PRELIMINARY; PRT: 2333 AA.
 AC 089089;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE PORE-FORMING CALCIUM CHANNEL ALPHA-1B SUBUNIT VARIANT A.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-NEURONAL;
 RX MEDLINE-97163393; PubMed-9010213;
 RA Lin Z., Haus S., Edgerton J., Lipscombe D.;
 RT "Identification of functionally distinct isoforms of the N-type Ca2+
 channel in rat sympathetic ganglia and brain.";
 RL Neuron 18:153-166(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-NEURONAL;
 RX Schorge S., Gupta S., Lin Z., Lipscombe D.;
 RT Stabilization of the N channel alpha1b message by calcium entry
 through L channels.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF055477; AAC29043.1; -;
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR001682; -;
 DR INTERPRO: IPR002077; -;
 DR INTERPRO: IPR002111; -;
 DR PFAM: PF00520; ion.trans. 4.
 DR PRINTS: PRO0167; CACHANNEL.
 SO SEQUENCE 2333 AA; 261928 MW; 14FC8E180CB2AA2A2 CRC64;

Query Match 55.7%; Score 44; DB 11; Length 2333;
 Best Local Similarity 58.3%; Pred. No. 55;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAQPN-DPSASEHT 12
 Db 1065 GSQPSDPSTVH 1076

RESULT 10
 ID 090MF4 PRELIMINARY; PRT: 378 AA.
 AC 090MF4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE SMF PROTEIN (FRAGMENT).
 GN SMF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE-96230328; PubMed-8786123;
 RA Gaster J.M., Brody T., Pulido J.C., Businga T., Sunden S., Hu X.,
 RA Mastra S., Buetow K.H., Murray J.C., Sheffield V.C., Boguski M.,
 RA Dayk G.M., Hudson T.J.;
 RT "Development of a screening set for new (CAG/CTG)n dynamic
 mutations.";
 RL Genomics 32:75-85(1996).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE-97179223; PubMed-9027509;
 RA Andre C., Hampe A., Lachaine P., Martin E., Wang X.P., Manus V.,
 RA Hu W.X., Gallibert F.;
 RT "Sequence analysis of two genomic regions containing the KIT and the
 RT FMS receptor tyrosine kinase genes.";
 RL Genomics 39:216-226(1997).
 DR EMBL: U63963; AAB51697.1; -;
 FT NON_TER
 SO SEQUENCE 378 AA; 41829 MW; 2F961731227B3EBB CRC64;

Query Match 53.2%; Score 42; DB 4; Length 378;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 GAQPN-DPSASEHT 13
 Db 262 GLOPNRDPSPAGHS 276

RESULT 11
 ID 09PVD1 PRELIMINARY; PRT: 592 AA.
 AC 09PVD1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE KV3.1 POTASSIUM CHANNEL.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Gurantz D., Lautermilch N.J., Watt S.D., Spltzer N.C.;
 RT "Sustained upregulation in Embryonic Spinal Neurons of a KV3.1

```

RT Potassium Channel Gene Encoding a Delayed Rectifier Current.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF132853; AAD52813.1; -.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion_trans. 1.
DR PFAM: PF02214; K_tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
RW Ionic channel.
SQ SEQUENCE      592 AA;  66891 MW;  882FAA230BDD8E8 CRC64;

OY          1 GAOPNDPSASERTH 14
   |||::|||:
Db         351 GADPDDITGSKHTY 364

RESULT  12
O13657    PRELIMINARY;      PRT:      803 AA.
AC O13657;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE PROBABLE MEMBRANE PROTEIN YOL130W.
CN P106 OR SPBC27B12.12C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=972H-.
RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA Ogura K., Otsuma R., Kudoh Y., Yanaoigata M., Machida M., Zhang M.Q.;
RU Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=972H-.
RA Wood V., Rajadream M.A., Barrell B.G., Lauber J., Hilbert H.,
RA Duesterhoeft A.;
RU Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL, AB004538; BAA21447.1; -.
DR EMBL, AL021766; CAA16907.1; -.
DR EMBL, AB004539; BAA21448.1; -.
DR INTERPRO: IPR002523; -.
DR PFAM: PF01544; Cora. 1.
DR Hypothetical protein.
KW SEQUENCE      803 AA;  89396 MW;  5E1DB270D9D83572 CRC64;

Query Match           53.2%; Score 42; DB 3; Length 803;
Best Local Similarity 50.0%; Pred. No. 42;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY          4 PNDPSASERTH 14
   |||||:| |::
Db         418 PNDPSSSLHSN 428

RESULT  13
O06409    PRELIMINARY;      PRT:     1932 AA.
AC O06409;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
```

```

DE DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE CHROMOSOME XII COSMID 9576.
GN L9576.7.
OC Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
RA Berns V., Brucherer M., Delius H., Dubois E., Dusterhoft A.,
RA Etian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Nelzel D., Hilbert H., Hliger F., Kleine K., Kotler P.,
RA Louis E.J., Messenguy F., Mewes H.W., Mosga T., Mostl D.,
RA Muller-Auer S., Newkirk U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetleil D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhaesselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambuit J., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohsels J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII." ;
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Favalle A.;
RN Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Waterston R.;
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; U20939; AAB67508.1; -.
SQ SEQUENCE 1932 AA; 221561 MW; 1E9CEAAEFBD3F94 CRC64;

Query Match 53.2%; Score 42; DB 3; Length 1932;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
   I-I-I-I : I-I-I-I
Db 1913 GSOPNTNDSQKH 1926

RESULT 14
ID Q9P7C6 PRELIMINARY; PRT; 209 AA.
AC Q9P7C6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DNAI PROTEIN (FRAGMENT).
GN SPCC10H1.02.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL162771; CAB85447.1; -.
FT NON_TER 209
SQ SEQUENCE 209 AA; 25323 MW; 020E519442A56AA2 CRC64;
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:37:11 ; Search time 38.22 Seconds

(without alignments)
24.872 Million cell updates/sec

Title: US-09-273-217-3

Sequence: 1 GAQPNDSASEHHT 14

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR66:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	79	100.0	511	2 A46020	potassium channel
2	79	100.0	511	2 S07095	potassium channel
3	79	100.0	585	2 A39395	delayed rectifier
4	71	89.9	581	2 S17150	potassium channel
5	71	89.9	613	2 A39402	potassium channel
6	71	89.9	624	2 S22703	voltage-gated pota
7	52	65.8	273	2 T34672	probable gntc faml
8	47	59.5	325	2 T16995	probable cinnamyl-
9	47	59.5	625	2 S13919	potassium channel
10	45	57.0	214	2 E75613	hypothetical prote
11	44	55.7	2288	2 S41080	calcium channel al
12	44	55.7	2336	2 A45386	omega-conotoxin-se
13	42	53.2	803	2 T40036	hypothetical prote
14	42	53.2	1932	2 S53409	probable membrane
15	41	51.9	276	2 T45275	oxidoreductase of
16	40	50.6	1711	2 C71625	variant-specific s
17	40	50.6	6420	2 T30283	polyketide synthas
18	39	49.4	327	2 T10736	cinnamyl-alcohol d
19	39	49.4	339	2 S70218	slip protein - Sal
20	39	49.4	343	2 S70549	glycoprotein gc -
21	39	49.4	508	2 S54264	hypothetical prote
22	39	49.4	548	2 T14793	hypothetical prote
23	39	49.4	683	2 T34103	discovered protei
24	39	49.4	716	2 JCS763	purine utilization
25	39	49.4	1060	2 S54779	parasporeal crystal
26	39	49.4	1136	1 USBS81	reticulocyte-bind
27	39	49.4	2829	1 A42771	basic transactivat
28	38	48.1	114	2 G40511	Terminal flower1
29	38	48.1	177	2 T48411	

30	38	48.1	222	2 S76133	sensory transducti
31	38	48.1	286	2 T49505	hypothetical prote
32	38	48.1	296	2 B75555	probable lipase/es
33	38	48.1	350	2 T16576	hypothetical prote
34	38	48.1	361	2 S19552	potassium channel
35	38	48.1	386	2 T05691	multisubunit chn
36	38	48.1	402	2 T51606	probable 265 prote
37	38	48.1	405	2 T12317	265 proteasome reg
38	38	48.1	452	2 T40769	hypothetical prote
39	38	48.1	474	2 H82564	3-isopropylmalate
40	38	48.1	513	2 S52571	phosphoprotein pho
41	38	48.1	603	2 S27055	basic serine prote
42	38	48.1	679	2 A42073	potassium channel
43	38	48.1	767	2 S55618	hypothetical prote
44	38	48.1	769	2 S56346	Shaw type potassi
45	38	48.1	798	2 S20881	homeotic protein p

ALIGNMENTS

```

RESULT 1
A46020
potassium channel KCNC1 - human
N:Alternate names: potassium channel NGK2-KV4; Shaw-related potassium channel KV3.1
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 19-May-1994 #text_change 05-Nov-1999
C:Accession: A46020; A45072
R:Ried, T.; Rudy, B.; Vega-Saenz de Miera, E.; Lau, D.; Ward, D.C.; Sen, K.
Genomics 15, Rudy, B.; Vega-Saenz de Miera, E.; Lau, D.; Ward, D.C.; Sen, K.
A:Title: Localization of a highly conserved human potassium channel gene (NGK2-KV4; K
A:Reference number: A46020; MUID:93194190
A:Accession: A46020
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <RIB>
A:Cross-references: S56770; NID:9298602; PIDN:AA825764.1; PID:9298603
A:Note: sequence extracted from NCBI backbone (NCBIN:127271, NCBIPI:127272)
R:Grismer, S.; Ghanshani, S.; Dethlefs, B.; McPherson, J.D.; Wasmuth, J.J.; Guitman,
J. Biol. Chem. 267, 20971-20979, 1992
A:Title: The Shaw-related potassium channel gene, KV3.1, on human chromosome 11, enco
A:Reference number: A45072; MUID:93016011
A:Accession: A45072
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 244-475 <GRI>
A:Cross-references: GB:M96747; NID:9186672; PIDN:AAA59458.1; PID:9186673
A:Experimental source: Louckes lymphoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116151)
C:Genetics:
A:Gene: GDB:KCNC1
A:Cross-references: GDB:128082; OMIM:176258
A:Map position: 11p15.1-11p15.1
C:Keywords: alternative splicing; glycoprotein; potassium channel; transmembrane prot

Query Match 100.0%; Score 79; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAQPNDSASEHHT 14
Db 370 GAQPNDSASEHHT 383

RESULT 2
S07095
potassium channel protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 05-Nov-1999
C:Accession: S07095
R:Yokoyama, S.; Imoto, K.; Kawamura, T.; Higashida, H.; Iwabe, N.; Miyata, T.; Numa,
FEBS Lett. 259, 37-42, 1989

```

A:Title: Potassium channels from NG108-15 neuroblastoma-glioma hybrid cells. Primary str
A:Reference number: 507095; MUID:90092535
A:Accession: 507095
A:Molecule type: mRNA
A:Residues: 1-511 <YOK>
A:Cross-references: EMBL:Y07521; NID:g533997; PIDN:CAA68814.1; PID:g533998
C:Keywords: alternative splicing; membrane protein

Query Match 100.0%; Score 79; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 6.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
|||||
Db 370 GAOPNDPSASEHTH 383

RESULT 3
A:39395
N:Alternate names: potassium channel KV4, neuronal - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 05-Nov-1999
C:Accession: A39395; S22704; S19100
R:Luneau, C.J.; Williams, J.B.; Marshall, J.; Levitan, E.S.; Oliva, C.; Smith, J.S.; Ant
Proc. Natl. Acad. Sci. U.S.A. 88, 3932-3936, 1991
A:Title: Alternative splicing contributes to K(+) channel diversity in the mammalian cer
A:Reference number: A39395; MUID:91219486
A:Accession: A39395
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-585 <LUN>
A:Cross-references: GB:M68880; GB:M37845; NID:g205106; PIDN:AAA41501.1; PID:g205107
R:Rettig, J.; Munder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Kues,
EMBO J. 11, 2473-2486, 1992
A:Title: Characterization of a shw-related potassium channel family in rat brain.
A:Reference number: S22702; MUID:92331599
A:Accession: S22704
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-585 <RET>
A:Cross-references: EMBL:X62840; NID:g57652; PIDN:CAA44644.1; PID:g57653
C:Keywords: alternative splicing; glycoprotein; ion channel; leucine zipper; transmembr
F:11-209/Domain: transmembrane #status predicted <TM1>
F:245-266/Domain: transmembrane #status predicted <TM2>
F:278-298/Domain: transmembrane #status predicted <TM3>
F:310-328/Domain: transmembrane #status predicted <TM4>
F:345-364/Domain: transmembrane #status predicted <TM5>
F:415-436/Domain: transmembrane #status predicted <TM6>

Query Match 100.0%; Score 79; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 8e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
|||||
Db 370 GAOPNDPSASEHTH 383

RESULT 4
S17150
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S17150
R:Luneau, C.; Wiedmann, R.; Smith, J.S.; Williams, J.B.
FEBS Lett. 288, 163-167, 1991
A:Title: Shaw-like rat brain potassium channel cDNA's with divergent 3' ends.
A:Reference number: S17150; MUID:91348257
A:Accession: S17150
A:Molecule type: DNA

A:Residues: 1-581 <LUN>

Query Match 89.9%; Score 71; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHT 13
|||||
Db 407 GAOPNDPSASEHT 419

RESULT 5
A39402
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 08-Oct-1999
C:Accession: A39402
R:McCormack, T.; Vega-Saenz de Miera, E.C.; Rudy, B.
Proc. Natl. Acad. Sci. U.S.A. 88, 4060, 1991
A:Reference number: A39402; MUID:91219512
A:Contents: erratum
A:Accession: A39402
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-613 <MCC>
A:Cross-references: GB:M34052; NID:g206913; PIDN:AAA42142.1; PID:g206914

Query Match 89.9%; Score 71; DB 2; Length 613;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHT 13
|||||
Db 407 GAOPNDPSASEHT 419

RESULT 6
S22703
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S22703; A45292; S19099
R:Rettig, J.; Munder, F.; Stocker, M.; Lichtinghagen, R.; Mastiaux, F.; Beckh, S.; Ku
EMBO J. 11, 2473-2486, 1992
A:Title: Characterization of a shw-related potassium channel family in rat brain.
A:Reference number: S22702; MUID:92331599
A:Accession: S22703
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-624 <RET>
A:Cross-references: EMBL:X62839; NID:g57650; PIDN:CAA44643.1; PID:g57651
R:Rudy, B.; Kentros, C.; Welser, M.; Fritsling, D.; Serodio, P.; Vega-Saenz de Miera,
Proc. Natl. Acad. Sci. U.S.A. 89, 4603-4607, 1992
A:Title: Region-specific expression of a K+ channel gene in brain.
A:Reference number: A45292; MUID:92262488
A:Accession: A45292
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 594-624 <RUD>
A:Note: sequence extracted from NCBI backbone (NCBIN:102300, NCBI:P.102305)
C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
F:230-248/Domain: transmembrane #status predicted <TM1>
F:282-303/Domain: transmembrane #status predicted <TM2>
F:315-335/Domain: transmembrane #status predicted <TM3>
F:347-365/Domain: transmembrane #status predicted <TM4>
F:382-401/Domain: transmembrane #status predicted <TM5>
F:452-473/Domain: transmembrane #status predicted <TM6>

Query Match 89.9%; Score 71; DB 2; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 13: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13
|||||
Db 407 GAOPNDPSASEHT 419

RESULT 7
T34672
probable gntR family transcription regulator - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34672
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21552
A:Accession: T34672
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-273 <SAU>
A:Cross-references: EMBL:AL034446; PIDN:CAA22393.1; GSPDB:GN00070; SCODEB:SC1A9.23
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCODEB:SC1A9.23

Query Match 65.8%; Score 52; DB 2; Length 273;
Best Local Similarity 57.1%; Pred. No. 0.15;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 14
||:|:|:|
Db 43 GAEPDGPAREHT 56

RESULT 8
T16995
probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - apple tree
C:Species: Malus domestica (apple tree)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T16995
R:Lee, J.R.; An, G.; Kim, S.R.
submitted to the EMBL Data Library, March 1998
A:Description: Molecular characterization of a fruit preferential cDNA encoding a putative
A:Reference number: Z18641
A:Accession: T16995
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-325 <LEF>
A:Cross-references: EMBL:AF053084; NID:q2981474; PID:q2981475
A:Experimental source: cv. Fuji
C:Genetics:
A:Gene: CAD
C:Function:
A:Description: catalyzes the reversible oxidation of cinnamyl alcohol to cinnamacetald
A:Pathway: Lignin biosynthesis
C:Superfamily: dihydrokaempferol 4-reductase
C:Keywords: Lignin biosynthesis; NADP; oxidoreductase

Query Match 59.5%; Score 47; DB 2; Length 325;
Best Local Similarity 63.6%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 14
||||:|
Db 40 PNDPTKTEHL 50

RESULT 9
S13919
potassium channel protein Raw3 - rat
C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Nov-1999
C:Accession: S13919; S22702
R:Schoeter, K.H.; Ruppersberg, J.P.; Wunder, F.; Rettig, J.; Stocker, M.; Pongs, O.
FEBS Lett. 278, 211-216, 1991
A:Title: Cloning and functional expression of a TEA-sensitive A-type potassium channel
A:Reference number: S13919; MUID:91122287
A:Accession: S13919
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-625 <SCH>
A:Cross-references: EMBL:X62841; NID:q57648; PIDN:CAA44645.1; PID:q57649
R:Rettig, J.; Wunder, F.; Stocker, M.; Lichtenhagen, R.; Mastiaux, F.; Beckh, S.; Ku
EMBO J. 11, 2473-2486, 1992
A:Title: Characterization of a shaw-related potassium channel family in rat brain.
A:Reference number: S22702; MUID:9233159
A:Accession: S22702
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-625 <RET>
A:Cross-references: EMBL:X62841; NID:q57648; PIDN:CAA44645.1; PID:q57649
C:Keywords: glycoprotein; ion channel; leucine zipper; transmembrane protein
F:228-246/Domain: transmembrane #status predicted <TM1>
F:282-303/Domain: transmembrane #status predicted <TM2>
F:315-335/Domain: transmembrane #status predicted <TM3>
F:347-365/Domain: transmembrane #status predicted <TM4>
F:382-401/Domain: transmembrane #status predicted <TM5>
F:452-473/Domain: transmembrane #status predicted <TM6>
F:257,266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.5%; Score 47; DB 2; Length 625;
Best Local Similarity 53.8%; Pred. No. 2.9;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEHT 13
||:|:|:|
Db 407 GARSPDPRGNDHT 419

RESULT 10
E75613
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: E75613
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uitterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75613
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-214 <KMT>
A:Cross-references: GB:AE001862; GB:AE001825; NID:q6460468; PIDN:AAF12308.1; PID:q646
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0170
A:Map position: 2

Query Match 57.0%; Score 45; DB 2; Length 214;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAOPNDPSASEH 12
|||||
Db 129 GAOPQOPAAVEH 140

RESULT 11
S41080

Fri Feb 2 15:15:36 2001

us-09-273-217-3.rpr

Page 5

Job time: 86 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:38:02 ; Search time 45.64 Seconds

(without alignments)
10.489 Million cell updates/sec

Title: US-09-273-217-3

Perfect score: 79
Sequence: 1 GAQPNDBSASEHTH 14Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq 36:*

1: /SIDS1/gcgdata/geneSeq/geneSeq/AA1980.DAT:*
2: /SIDS1/gcgdata/geneSeq/geneSeq/AA1981.DAT:*
3: /SIDS1/gcgdata/geneSeq/geneSeq/AA1982.DAT:*
4: /SIDS1/gcgdata/geneSeq/geneSeq/AA1983.DAT:*
5: /SIDS1/gcgdata/geneSeq/geneSeq/AA1984.DAT:*
6: /SIDS1/gcgdata/geneSeq/geneSeq/AA1985.DAT:*
7: /SIDS1/gcgdata/geneSeq/geneSeq/AA1986.DAT:*
8: /SIDS1/gcgdata/geneSeq/geneSeq/AA1987.DAT:*
9: /SIDS1/gcgdata/geneSeq/geneSeq/AA1988.DAT:*
10: /SIDS1/gcgdata/geneSeq/geneSeq/AA1989.DAT:*
11: /SIDS1/gcgdata/geneSeq/geneSeq/AA1990.DAT:*
12: /SIDS1/gcgdata/geneSeq/geneSeq/AA1991.DAT:*
13: /SIDS1/gcgdata/geneSeq/geneSeq/AA1992.DAT:*
14: /SIDS1/gcgdata/geneSeq/geneSeq/AA1993.DAT:*
15: /SIDS1/gcgdata/geneSeq/geneSeq/AA1994.DAT:*
16: /SIDS1/gcgdata/geneSeq/geneSeq/AA1995.DAT:*
17: /SIDS1/gcgdata/geneSeq/geneSeq/AA1996.DAT:*
18: /SIDS1/gcgdata/geneSeq/geneSeq/AA1997.DAT:*
19: /SIDS1/gcgdata/geneSeq/geneSeq/AA1998.DAT:*
20: /SIDS1/gcgdata/geneSeq/geneSeq/AA1999.DAT:*
21: /SIDS1/gcgdata/geneSeq/geneSeq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	14	20	Y42764 Rat potassium chan
2	71	89.9	601	20	Y34120 Human potassium ch
3	47	59.5	270	17	R91952 Lung cancer specif
4	47	59.5	274	17	R91953 Lung cancer specif
5	47	59.5	325	17	R91951 Lung cancer specif
6	47	59.5	325	17	R91955 Lung cancer specif
7	47	59.5	354	17	R91950 Lung cancer specif
8	44	55.7	434	17	R96419 Peptide fragment o
9	40	50.6	1574	21	Y84729 Amino acid sequenc
10	39	49.4	338	18	W15270 Salmonella secreta
11	39	49.4	603	14	R44004 Basic protease. D
12	39	49.4	1095	10	P97052 Sequence encoded b

13	39	49.4	1136	9	P82314 Bacillus thuringie
14	39	49.4	1136	10	P93341 Sequence encoded b
15	39	49.4	1178	7	P60051 Sequence of insect
16	39	49.4	2427	21	Y51843 Murine embryo macr
17	38	48.1	98	15	R63235 CNS neural thread
18	38	48.1	98	17	R95914 HB4 human neural t
19	38	48.1	177	18	W13945 Arabidopsis termin
20	38	48.1	202	20	Y35338 Chlamydia pneumoni
21	38	48.1	513	9	P81501 Basic serine prote
22	38	48.1	1788	21	Y85575 D. melanogaster BA
23	38	48.1	2071	21	Y84686 Amino acid sequenc
24	37	46.8	14	21	Y81320 Human growth hormo
25	37	46.8	163	30	Y29213 Amino acid sequenc
26	37	46.8	181	18	W13944 Antirrhinum centro
27	37	46.8	266	20	Y43944 Yeast protein kina
28	37	46.8	267	20	Y43946 Fission yeast prot
29	37	46.8	285	20	Y34849 Chlamydia pneumoni
30	36	45.6	131	20	Y60109 Human endometrium
31	36	45.6	159	18	W50288 Human Fas antigen
32	36	45.6	160	20	Y48363 Human prostate can
33	36	45.6	246	19	W77312 Polypeptide sequen
34	36	45.6	328	21	Y54617 Arabidopsis Abi4 p
35	36	45.6	376	18	W50287 Human Fas antigen
36	36	45.6	376	19	W60037 Antigenic peptide
37	36	45.6	396	18	W18574 Aggrease artififi
38	36	45.6	396	18	W18575 Aggrease artififi
39	36	45.6	403	20	Y43174 Mouse cyclin E2 pr
40	36	45.6	497	21	Y74865 Neisseria meningit
41	36	45.6	497	21	Y75810 Neisseria meningit
42	36	45.6	497	21	Y75882 P/C protein of atc
43	36	45.6	507	14	R34538 Fructosyltransfera
44	36	45.6	543	16	R79142 Human P1A3 protei
45	36	45.6	584	20	Y29619

ALIGNMENTS

RESULT 1
ID Y42764 standard; peptide; 14 AA.
AC Y42764:
XX 20-DEC-1999 (first entry)
XX Rat potassium channel Kv3.1 vestibule-derived peptide #3.
DE Ion channel; potassium channel; vestibule; inhibitor; antibody;
KW polyclonal; antagonist; hypertension; cardiac ischemia;
KW bronchial constriction; neurological diseases.
XX
OS Synthetic.
OS Rattus sp.
XX
XX W09948927-A1.
PN
XX 30-SEP-1999.
PD
XX 19-MAR-1999; 99WO-US06019.
PF
XX 25-MAR-1998; 98US-0079268.
PR
XX (CORR) CORNELL RES FOUND INC.
PA
XX Huang X:
PI WPI: 1999-601205/51.
DR Designing specific blockers that bind to the external vestibule region
XX of ion channels, potentially useful for treating e.g. hypertension -
PT Claim 9; Page 8; 40pp; English.
PS

XX This sequence represents a peptide (#3), derived from the
 CC extracellular vestibule portion of the rat potassium channel Kv3.1.
 CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
 CC generate polyclonal antibodies. The vestibule portion of potassium
 CC channels is located on the extracellular portion of the channel protein,
 CC and generally comprises a loop between the S5 transmembrane domain and
 CC the pore forming region of the channel, or between the pore forming
 CC region and the S6 transmembrane domain. The antibodies generated against
 CC vestibule peptides act as potassium channel inhibitors by binding to the
 CC vestibule portion, physically blocking the pore, or otherwise inducing a
 CC conformational change in the channel. These potassium channel blockers
 CC are potential therapeutic agents for e.g., hypertension, cardiac
 CC ischemia, bronchial constriction and neurological diseases. Such
 CC inhibitors are specific for particular types of ion channel, and
 CC are produced by rational design based on known nucleotide and amino acid
 CC sequences for ion channels.

XX Sequence 14 AA:

SQ

Query Match 100.0%; Score 79; DB 20; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHTH 14
 Db 1 gaopndpsasehth 14

RESULT 2
 Y34120
 ID Y34120 standard; Protein; 601 AA.

AC Y34120;

XX 30-NOV-1999 (first entry)

DE Human potassium channel K+Hnov4.

XX Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;

KM cardiovascular disorder; CNS disorder; renal disorder.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 103 /note="Ala substituted by Thr in a variant form of
 FT K+Hnov4"

XX MO9943696-A1.

XX 02-SEP-1999.

XX 22-FEB-1999; 99MO-US03826.

XX 19-JAN-1999; 99US-0116448.

XX 25-FEB-1998; 98US-0076687.

XX 07-AUG-1998; 98US-0095836.

XX (AXYS-) AXYS PHARM INC.

XX Curran ME, Hu P, Miller AP, Rutter M, Wang J;

XX WPI: 1999-527591/44.

XX N-PSDB; Y34120.

XX New nucleic acids encoding mammalian K+Hnov potassium channel
 PT proteins, useful for the diagnosis and treatment of episodic ataxia
 PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
 XX
 PS Claim 3; Page 48-49; 112pp; English.

CC This sequence represents the human K+Hnov4 potassium channel.
 CC K+Hnov proteins have a high degree of homology to known potassium
 CC channels and may be alpha subunits, which form the functional channel,
 CC or accessory subunits that act to modulate the channel activity.
 CC K+Hnov4 is a voltage gated potassium channel. K+Hnov cDNAs were
 CC isolated by extension of expressed sequence tags (ESTs) which were
 CC related but not identical to known human potassium channels. Potential
 CC polymorphisms detected as sequence variants between multiple
 CC independent clones. Potassium channels have critical roles in various
 CC cell types and biochemical pathways. Defective potassium channels are
 CC known to cause four human diseases: episodic ataxia with myokymia,
 CC cardiac arrhythmia (Long QT syndrome); epilepsy; and Bartter's syndrome.
 CC As potassium channels are critical components of virtually all cells,
 CC it is likely that abnormal potassium channels are also implicated in
 CC certain renal, cardiovascular and central nervous system (CNS) disorders.
 CC Nucleotides encoding K+Hnov proteins may be used for identifying
 CC homologous or related proteins and the DNA sequences encoding them. They
 CC may be used to produce compositions that modulate the expression and
 CC function of the K+Hnov protein and in studying the biochemical pathways
 CC associated with it. They may also be used for the recombinant production
 CC of K+Hnov protein in fermentation cultures. Additionally, such
 CC nucleotides may be used in gene therapy protocols for the treatment
 CC of diseases associated with abnormal potassium channels.

SQ Sequence 601 AA:

Query Match 89.9%; Score 71; DB 20; Length 601;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAOPNDPSASEHT 13
 Db 371 gaopndpsaseht 383

RESULT 3
 R91952
 ID R91952 standard; Protein; 270 AA.

AC R91952;

XX 23-APR-1996 (first entry)

DE Lung cancer specific antigen HCAVIII truncated protein.

XX Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;

KM carbonic anhydrase; diagnosis; therapy; antibody; ELISA.

XX Synthetic.

XX MO9602552-A1.

XX 01-FEB-1996.

XX 19-JUL-1995; 95MO-US09145.

XX 19-JUL-1994; 94US-0276919.

XX (CYTO-) CYTOCLONAL PHARM INC.

XX Bolton AP, Torczynski RM;

XX WPI: 1996-105844/11.

XX N-PSDB; T15450.

XX Nucleic acid encoding the lung cancer specific antigen HCAVIII
 PT useful for diagnosis and treatment of non-small cell lung cancer
 XX
 PS Claim 9; Page 53-54; 87pp; English.

CC Truncated forms (R91952-53) of HCAVIII, lacking the membrane spanning
 CC fragment and the intracellular domain, were produced in Escherichia

CC cells transformed with a vector carrying the encoding cDNA (see
 CC T15450 and T15451). HCAVIII is a cell surface antigen which is
 CC highly specific for non-small cell lung carcinoma (NSCLC) and which
 CC has features in common with human carbonic anhydrases. The
 CC truncated HCAVIII is more accurate representations of the putative
 CC HCAVIII shed antigen found in biopsy specimens and may be the
 CC preferred antigens for polyclonal antisera and monoclonal antibody
 CC prepn. for use in ELISA test development.

XX Sequence 270 AA;

Query Match

Best Local Similarity 59.5%; Score 47; DB 17; Length 270;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 DB 95 pndpghseht 104

RESULT 4

R91953 R91953 standard; Protein; 274 AA.

XX AC R91953;

DT 23-APR-1996 (first entry)

DE Lung cancer specific antigen HCAVIII truncated protein.

KM Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
 KM carbonic anhydrase; diagnosis; therapy; antibody; ELISA.

OS Synthetic.

PN W09602552-A1.

PD 01-FEB-1996.

PF 19-JUL-1995; 95WO-US09145.

PR 19-JUL-1994; 94US-0276919.

PA (CYTO-) CYTOCLONAL PHARM INC.

PI Bolton AP, Torczynski RM;

DR WPI: 1996-105844/11.

DR N-PSDB; T15451.

PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
 PT useful for diagnosis and treatment of non-small cell lung cancer
 PS Claim 11; Page 56-57; 87pp; English.

XX Truncated forms (R91952-53) of HCAVIII, lacking the membrane spanning
 CC fragment and the intracellular domain, were produced in Escherichia
 CC cells transformed with a vector carrying the encoding cDNA (see
 CC T15450 and T15451). HCAVIII is a cell surface antigen which is
 CC highly specific for non-small cell lung carcinoma (NSCLC) and which
 CC has features in common with human carbonic anhydrases. The
 CC truncated HCAVIII is more accurate representations of the putative
 CC HCAVIII shed antigen found in biopsy specimens and may be the
 CC preferred antigens for polyclonal antisera and monoclonal antibody
 CC prepn. for use in ELISA test development.

XX Sequence 274 AA;

Query Match 59.5%; Score 47; DB 17; Length 274;
 Best Local Similarity 80.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 DB 96 pndpghseht 105

RESULT 5

R91951 R91951 standard; Protein; 325 AA.

XX AC R91951;

DT 23-APR-1996 (first entry)

DE Lung cancer specific antigen HCAVIII mature protein.

KM Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
 KM carbonic anhydrase; diagnosis; therapy; antibody.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 51 /label= N-glycosylation_site

FT Modified-site 133 /label= N-glycosylation_site

FT Modified-site 151 /label= N-glycosylation_site

FT Modified-site 202 /label= N-glycosylation_site

FT Modified-site 895..906 /label= N-glycosylation_site

FT /note= "phosphorylation site is recognised by
 FT protein kinase C and other kinases"

PN W09602552-A1.

PD 01-FEB-1996.

PF 19-JUL-1995; 95WO-US09145.

PR 19-JUL-1994; 94US-0276919.

PA (CYTO-) CYTOCLONAL PHARM INC.

PI Bolton AP, Torczynski RM;

DR WPI: 1996-105844/11.

DR N-PSDB; T15449.

PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
 PT useful for diagnosis and treatment of non-small cell lung cancer
 PS Claim 7; Page 44-46; 87pp; English.

XX The mature HCAVIII protein (R91951) was produced as a GST fusion in
 CC Escherichia coli cells transformed with the encoding cDNA (T15449)
 CC cloned into pGEX4T-1. It was isolated by affinity purification and
 CC thrombin cleavage. HCAVIII is a cell surface antigen which is
 CC highly specific for non-small cell lung cancer, and which shares
 CC regions of homology with human carbonic anhydrases. It can be used
 CC to produce antibodies of therapeutic or diagnostic application.

XX Sequence 325 AA;

Query Match 59.5%; Score 47; DB 17; Length 325;
 Best Local Similarity 80.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
 DB 96 pndpghseht 105

```

RESULT 6
R91955
ID R91955 standard; Protein; 325 AA.
XX
AC R91955;
XX
DT 23-APR-1996 (first entry)
XX
DE HCAVIII phosphorylation-modified (S3026) protein.
XX
KM Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
KW carbonic anhydrase; diagnosis; therapy; antibody;
XX phosphorylation.
XX
OS Synthetic.
XX
PN W09602552-A1.
XX
PD 01-FEB-1996.
XX
PE 19-JUL-1995; 95WO-US09145.
XX
PR 19-JUL-1994; 94US-0276919.
XX
PA (CYTO-) CYTOCLONAL PHARM INC.
XX
PI BOLLON AP, Torczynski RM;
XX
DR WPI: 1996-105844/11.
DR N-PSDB; T15454.
XX
PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
PT useful for diagnosis and treatment of non-small cell lung cancer
XX
PS Claim 16; Page 59-60; 87pp; English.
XX
XX A cDNA sequence (T15454) codes for a phosphorylation-modified form
CC (R91955) of HCAVIII, a cell surface antigen which is highly
CC specific for non-small cell lung carcinoma (NSCLC) and which has
CC features in common with human carbonic anhydrases. The modified
CC HCAVIII has glycine substituted for serine at position 302 of the
CC mature protein. It is used to study the role of HCAVIII serine
CC phosphorylation in oncogenesis.
XX
SQ Sequence 325 AA;

```

```

Query Match 59.5%; Score 47; DB 17; Length 325;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 PNDPSASEHT 13
Db 96 pndpghseht 105

```

```

RESULT 7
R91950
ID R91950 standard; Protein; 354 AA.
XX
AC R91950;
XX
DT 23-APR-1996 (first entry)
XX
DE Lung cancer specific antigen HCAVIII pre-protein.
XX
KM Non-small cell lung cancer; NSCLC; tumour marker; HCAVIII;
KW carbonic anhydrase; diagnosis; therapy; antibody.
XX
OS Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT Modified-site 28
FT /label= N-glycosylation_site
FT Peptide 1..29
FT /label= Sig-peptide
FT Protein 30..354
FT /label= Mat-protein
FT Modified-site 80
FT /label= N-glycosylation_site
FT Modified-site 162
FT /label= N-glycosylation_site
FT Modified-site 180
FT /label= N-glycosylation_site
FT Modified-site 231
FT /label= N-glycosylation_site
FT Modified-site 328..331
FT /label= Phosphorylation_site
FT /note= "the phosphorylation site recognised by
protein kinase C and other kinases"

```

```

W09602552-A1.
XX
PD 01-FEB-1996.
XX
PE 19-JUL-1995; 95WO-US09145.
XX
PR 19-JUL-1994; 94US-0276919.
XX
PA (CYTO-) CYTOCLONAL PHARM INC.
XX
PI BOLLON AP, Torczynski RM;
XX
DR WPI: 1996-105844/11.
DR N-PSDB; T15448.
XX
PT Nucleic acid encoding the lung cancer specific antigen HCAVIII -
PT useful for diagnosis and treatment of non-small cell lung cancer
XX
PS Claim 1; Page 41-42; 87pp; English.
XX
XX The pre-protein (R91950) of a cell surface antigen highly specific
CC for non-small cell lung carcinoma, HCAVIII, is the product of a
CC cDNA sequence (T15448) in vector pLC56. HCAVIII has some features
CC in common with 7 previously known human carbonic anhydrases.
CC The HCAVIII mature protein (R91951) and truncated HCAVIII lacking
CC the transmembrane domain (R91952-53) have been expressed in
CC Escherichia coli and used to raise antibodies for diagnostic and
CC therapeutic applications.
XX
SQ Sequence 354 AA;

```

```

Query Match 59.5%; Score 47; DB 17; Length 354;
Best Local Similarity 80.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 PNDPSASEHT 13
Db 125 pndpghseht 134

```

```

RESULT 8
R96419
ID R96419 standard; peptide; 434 AA.
XX
AC R96419;
XX
DT 11-NOV-1996 (first entry)
XX
DE Peptide fragment of N-type calcium channel.
XX
KM Calcium channel; synapse; synaptic vesicle; presynaptic; syntaxin;
KW synaptosome; neuronal cell death; ischaemia; stroke; epilepsy;
XX

```

KW	cognitive deficit; inhibition; screening; detection; treatment.
XX	
OS	Rattus rattus.
XX	
XX	Key
XX	Region
XX	Location/Qualifiers
XX	718..1141
XX	/note="Claimed peptide region."
XX	
PN	W09615149-A2.
XX	
PD	23-MAY-1996.
XX	
PE	09-NOV-1995; 95WO-US14776.
XX	
PR	10-NOV-1994; 94US-0337602.
PA	(UNIMW) UNIV WASHINGTON.
PI	Catterall WA, Sheng Z;
XX	
XX	WP1; 1996-259782/26.
DR	
PT	Screening for presynaptic calcium channel blockers - identifies
PT	compounds which inhibit docking of presynaptic vesicles to calcium
PT	channels, rather than compounds which inhibit calcium influx
XX	
XX	Claim 7; Figure 11A; 53pp; English.
PS	
XX	
CC	A method of screening for compounds that inhibit the interaction
CC	between presynaptic calcium channels and presynaptic vesicles
CC	comprises contacting calcium channel-like peptide with a candidate
CC	compound under conditions sufficient to permit binding between the
CC	peptide and the candidate compound, where the peptide is able to
CC	bind syntaxin or synaptosome associated protein, and then detecting
CC	the presence or absence of binding between the peptide and the
CC	candidate compound, thereby determining whether the candidate
CC	compound bound to the peptide. The method allows for the screening
CC	of compounds which inhibit the docking of presynaptic vesicles to
CC	calcium channels and which therefore prevent neurotransmitter release
CC	by binding to a selected presynaptic calcium channel-like peptide.
CC	Isolated compounds may be used in the prevention of neuronal cell
CC	death that accompanies cerebral ischemia. They may also be used in
CC	the treatment of stroke, cognitive deficit related to cardiac
CC	surgery and neuronal damage caused during acute epileptic episodes.
CC	This sequence corresponds to the LII-III loop (amino acids 710-1143
CC	of the rat N-type calcium channel.
CC	
XX	
SO	Sequence 434 AA;
	Query Match 55.7%; Score 44; DB 17; Length 434;
	Best Local Similarity 58.3%; Pred. No. 9.1';
	Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY	1 GAQPNDPASSEH 12
	1:11:111 : 1
DB	357 gsqpsdpsctvth 368
RESULT 9	
ID Y84729	Y84729 standard; Protein: 1574 AA.
XX AC	Y84729;
XX DT	08-AUG-2000 (first entry)
XX DE	Amino acid sequence of FK-520 PKs gene cluster module 8.
XX KW	FK-520: polypeptide synthase; PKs: gene cluster; immunosuppressant;
XX KW	immunophilin; FK-506 binding protein; polypeptide compound; uvelitis;
XX KW	transplant rejection; graft-versus-host disease; alopecia universalis;
KW	autoimmune chronic active hepatitis; inflammatory bowel disease;

XX	multiple sclerosis; primary biliary cirrhosis; scleroderma;
KW	neurite outgrowth; nerve regrowth; Parkinson's disease;
KW	Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
KW	peripheral neuropathy.
XX	
OS	Streptomyces hygroscopicus.
XX	
PN	W0200020601-A2.
XX	
PD	13-APR-2000.
XX	
XX	
PE	01-OCT-1999; 99WO-US22886.
XX	
XX	
PR	02-OCT-1998; 98US-0102748.
PR	11-MAR-1999; 99US-0123810.
PR	17-JUN-1999; 99US-0139650.
XX	
PA	(KOSA-) KOSAN BIOSCIENCES INC.
XX	
PI	Reeves C, Chu D, Khosla C, Sauti D, Wu K;
DR	WPI; 2000-317716/27.
DR	N-PSDB; A14665.
XX	
PT	New isolated polyketide synthase nucleic acid and polyketide compounds,
PT	useful for treating e.g. transplant rejection, uveitis, multiple
PT	sclerosis, Alzheimer's disease, Parkinson's disease, stroke, or
PT	peripheral neuropathy -
XX	
PS	Example 2; Page 90-93; 126pp; English.
XX	
CC	The present sequence represents module 8 of the FK-520 polyketide
CC	synthase (PKS) gene cluster of strain M6548. FK-506 is a potent
CC	immunosuppressant, and acts through initial formation of an
CC	intermediate complex with protein immunophilins known as FK-506
CC	binding proteins. The nucleic acids are used for producing polyketide
CC	compounds. The polyketide compounds can be used as immunosuppressants to
CC	prevent or treat transplant rejection, graft-versus-host disease or
CC	uveitis. They can also be used for treating e.g. alopecia universalis,
CC	autoimmune chronic active hepatitis, inflammatory bowel disease,
CC	multiple sclerosis, primary biliary cirrhosis, or scleroderma. They
CC	also have neurotrophic activity and can be used to promote neurite
CC	outgrowth in NGF-treated PC12 cells and in sensory neuronal cultures,
CC	and in intact animals, they promote regrowth of damaged facial and
CC	sciatic nerves, and repair lesioned serotonin and dopamine neurons in
CC	the brain. They can also be used for treating e.g. Parkinson's disease,
CC	Alzheimer's disease, stroke, traumatic spinal cord and brain injury, or
CC	peripheral neuropathies. They can also be used in agricultural and
CC	veterinary applications.
XX	
SQ	Sequence 1574 AA;
XX	
QY	4 PNDPSASEHT 13
DB	1111: 1111
DB	722 pndpsrsght 731
XX	
RESULT 10	
W15270	
ID	W15270 standard; Protein: 338 AA.
XX	
AC	W15270:
XX	
DT	04-AUG-1997 (first entry)
XX	
DE	Salmonella secreted protein SspD.
XX	
KW	Salmonella secreted protein; SspD; bacterial-mediated endocytosis;

KM diagnosis: therapy; vaccine; attenuation; virulence.
 XX
 OS Salmonella typhimurium.
 XX
 FH Key
 FT 1.338 Location/Qualifiers
 FT /note= "the amino acid sequence does not fully
 correspond to the translated sequence of
 the sspD gene of Fig 21"
 FT
 XX
 PN MO9718225-A1.
 XX
 PD 22-MAY-1997.
 XX
 PE 14-NOV-1996; 96WO-US18504.
 XX
 PR 14-NOV-1995; 95US-0006733.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Miller SI.
 XX
 DR WPI: 1997-289217/26.
 DR N-PSDB: T67030.
 XX
 PT New isolated Salmonella secreted proteins and related genes - used
 PT to develop products for the detection, treatment or prevention of
 PT Salmonella infections
 XX
 PS Claim 24; Fig 14; 95pp; English.
 XX
 CC Salmonella secreted proteins SspB, SspC, SspD and SspA (W15268-71)
 CC are virulence factors involved (except SspA) in bacterial
 CC mediated endocytosis, and are able to translocate into human
 CC epithelial cells. Ssp secretion is dependent on the expression
 CC of prgH (see also T67036). Ssp genes (T67028-31) were isolated
 CC by examining S. typhimurium mutants in invasion assays on HEP-2
 CC epithelial cells. Ssp polypeptides can be used in methods for the
 CC detection, treatment or prevention of Salmonella infection.
 CC Chemeric proteins incorporating Ssp can be used to target an
 CC antigen to epithelial cells or to induce a cytotoxic T cell
 CC response in a mammal. Decreased secretion of Ssp provides
 CC attenuated bacterial cells suitable as live vaccines.
 XX
 SQ Sequence 338 AA;
 Query Match 49.4%; Score 39; DB 18; Length 338;
 Best Local Similarity 70.0%; Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 3 QPNDSASEH 12
 : | | | | | | |
 Db 19 rpgtspaseh 28
 RESULT 11
 ID R44004 standard; Protein; 603 AA.
 XX
 AC R44004;
 XX
 DT 13-MAY-1994 (first entry)
 XX
 DE Basic protease.
 XX
 KM Acid protease; isoenzyme; D. nodosus; benign; strain 305; epitope; V1;
 KM basic protease; diagnosis; detection; virulent; intermediate; vaccine;
 KM antibody; V2; G100P1; B2; foot rot; detergent; domestic; dairy; food;
 KM textile; leather; pharmaceutical; medical; cosmetic; veterinary.
 XX
 OS Dichelobacter nodosus benign strain 305.

PN GB2267148-A.
 XX
 PD 24-NOV-1993.
 XX
 PE 04-MAY-1993; 93GB-0009159.
 XX
 PR 01-MAY-1992; 92AU-0002226.
 PR 10-JUL-1992; 92AU-0003445.
 PR 14-SEP-1992; 92AU-0004708.
 PR 14-SEP-1992; 92AU-0004711.
 PR 10-DEC-1992; 92AU-0006284.
 PR 14-JAN-1993; 93AU-0006827.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Edwards RD, Focareta A, Kortt AA, Lilley GG, Riffkin MC;
 PI Stewart DJ, Vaughan JA, Wang L, Wang LF;
 XX
 DR WPI: 1993-353826/45.
 DR N-PSDB: Q51275.
 XX
 PT Ovine foot rot infection diagnostic assay for rapid strain
 PT differentiation - by detecting epitope(s) and/or antibodies
 PT specific to epitope in virulent, benign, and/or intermediate
 PT strains, for protease vaccine and deoxyribonucleic acid
 XX
 PS Claim 36; Fig 4; 103pp; English.
 XX
 CC This sequence represents the basic protease from the D.
 CC nodosus benign strain 305. Epitopes found on acidic or basic
 CC proteases may be used in the diagnostic method of the invention.
 CC The method involves detecting at least one of:
 CC (i) an epitope present in virulent and/or at least some
 CC intermediate strains but not in benign strains;
 CC (ii) an epitope present in benign and/or at least some
 CC intermediate strains but not in virulent strains;
 CC (iii) an epitope present in some intermediate strains but not
 CC in virulent, or most benign strains; or
 CC (iv) antibodies specific to these epitopes.
 CC Epitopes in class (i) are pref. present on V2 or G100P1, class (ii)
 CC are pref. present on B2 and class (iii) are pref. present on V1. D.
 CC nodosus proteases are useful in vaccines for the control of foot rot,
 CC eg. as an additive to known vaccines based on basic proteases. Hybrid
 CC proteases can serve as carriers of foreign epitopes. The proteases
 CC can be used as detergents for domestic, dairy, food, textile, leather,
 CC pharmaceutical, medical, cosmetic and veterinary purposes.
 XX
 SQ Sequence 603 AA;
 Query Match 49.4%; Score 39; DB 14; Length 603;
 Best Local Similarity 53.8%; Pred. No. 94;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 2 AOPNDSASEH 14
 : | | | | | : |
 Db 133 aapndpsyqgwh 145
 RESULT 12
 ID P97052 standard; protein; 1095 AA.
 XX
 AC P97052;
 XX
 DT 23-DEC-1990 (first entry)
 XX
 DE Sequence encoded by insecticide gene from Bacillus thuringiensis
 DE israelensis strain.
 XX
 KM Insecticide; diptera larvae; aedes.
 XX
 OS Bacillus thuringiensis.

XX JP01080294-A.
 PN 27-MAR-1989.
 PD 21-SEP-1987; 87JP-0238394.
 PF 21-SEP-1987; 87JP-0238394.
 PR 21-SEP-1987; 87JP-0238394.
 XX (MARU-) MARUBENI KK.
 PA (SUMO) SUMITOMO CHEMICAL IND. KK.
 DR WPI: 1989-134798/18.
 DR N-PSDB: N92515.
 XX Insecticide protein gene -
 PT from *Bacillus thuringiensis israelensis* strain, used to produce
 PT protein toxic to diptera larvae, e.g. aedes
 PS Disclosure: Fig 2-1 to 2-3; 8pp; Japanese.
 CC The protein gene has high insecticide activity to diptera
 CC larvae such as aedes.
 CC Sequence 1095 AA;
 SQ

Query Match 49.4%; Score 39; DB 10; Length 1095;
 Best Local Similarity 45.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 OY 4 PNDPSASETH 14
 || | : : : ||
 Db 392 pnpptvndyth 402

RESULT 13
 P82314
 ID P82314 standard; protein; 1136 AA.
 AC P82314;
 XX 13-NOV-1990 (first entry)
 DT 13-NOV-1990 (first entry)
 XX *Bacillus thuringiensis* 8 protein.
 DE *Bacillus thuringiensis* 8 protein.
 XX Bt 8 protein; insecticides; mosquitos.
 KM W08806631-A.
 PN 07-SEP-1988.
 XX 07-SEP-1988.
 PD 03-MAR-1988; 88WO-US00734.
 XX 04-MAR-1987; 87US-0021405.
 PR (UNMS) MICHIGAN STATE UNIV.
 XX (PLAN-) PLANT GENETIC SYST.
 PA (UNMI) UNIV OF MICHIGAN.
 PA Vaack MA, Chungjatupornchai W, McIntosh L;
 PI WPI: 1988-271170/38.
 DR N-PSDB: N62106.
 DR Chimeric gene for expression in *Cyanobacteria* - contg. DNA fragment
 PT coding for insecticidal active protein produced by *Bacillus* strain.
 PS Disclosure: P; English.
 CC The corresp. gene is ligated to a promoter region enabling ex-
 CC pression in *Cyanobacteria* and the resultant chimeric gene is used
 CC to produce this Bt 8 protein. A truncated form of the protein can

CC also be produced using a shorter gene. Transformed *Cyanobacteria*
 CC and their progeny can be used in insecticidal compsns., esp. for
 CC controlling mosquitos.
 CC Sequence 1136 AA;
 SQ

Query Match 49.4%; Score 39; DB 9; Length 1136;
 Best Local Similarity 45.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 OY 4 PNDPSASETH 14
 || | : : : ||
 Db 433 pnpptvndyth 443

RESULT 14
 P93341
 ID P93341 standard; protein; 1136 AA.
 AC P93341;
 XX 27-JAN-1991 (first entry)
 DT 27-JAN-1991 (first entry)
 XX Sequence encoded by toxin gene derived from a *Bacillus thuringiensis* var.
 DE *israelensis* (B.t.i.) microbe identified as strain HD567.
 XX Insecticide; diptera; mosquito.
 KM *Bacillus thuringiensis*.
 OS *Bacillus thuringiensis*.
 XX EP308199-A.
 PN 22-MAR-1989.
 PD 14-SEP-1988; 88EP-0308498.
 PF 16-JUN-1988; 88US-0207690.
 PR (MYCO-) MYCOGEN CORP.
 XX Gilroy TE;
 XX WPI: 1989-087579/12.
 DR N-PSDB: N91003.
 XX *Bacillus thuringiensis* toxin toxic to dipteran insects -
 PT produced by gene isolated from *Bacillus thuringiensis* var.
 PT *israelensis* strain
 XX Claim 1; pp 7-10; 13pp; English.
 PS A toxin active against dipteran insects, having a specified aa sequence
 CC or a mutant having the same protein secondary structure or, if the
 CC structure is altered, having the same biological activity, is claimed.
 CC Also claimed is a DNA molecule including a nucleotide sequence encoding
 CC the aa sequence. The novel toxin gene is toxic to dipteran insects e.g.
 CC mosquitos.
 CC Sequence 1136 AA;
 SQ

Query Match 49.4%; Score 39; DB 10; Length 1136;
 Best Local Similarity 45.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 OY 4 PNDPSASETH 14
 || | : : : ||
 Db 433 pnpptvndyth 443

RESULT 15
 P60051

ID P60051 standard; Protein; 1178 AA.
XX
AC P60051;
XX
DT 06-SEP-1991 (first entry)
XX
DE Sequence of insecticidal protein related to bacterial delta
XX endotoxin encoded by VBI31 clone circular plasmid obtained from
XX the Bacillus thuringiensis var. israelensis.
KM Insecticide; microbial.
XX
OS Bacillus thuringiensis.
XX
PN EP195285-A.
XX
PD 24-SEP-1986.
XX
PE 27-FEB-1986; 86EP-0102547.
XX
PR 28-FEB-1985; 85US-0706836.
XX
PA (UYGE-) UNIV GEORGIA RES.
XX
PI Sekar VS, Carlton BD;
XX
DR WPI; 1986-253299/39.
XX
DR N-PSDB; N60055.
XX
PT Insecticidal protein related to bacterial delta-endotoxin - is
PT obtd. by recombinant DNA methods from transform microorganism
XX
PS Claim 28; Fig 8; 69pp; English.
XX
CC The patentors claim a toxic protein having an amino portion
CC identical to the amino portion of delta-endotoxin from Bacillus
CC thuringiensis var. israelensis and a carboxy-terminus portion
CC different from the carboxy portion of the delta-endotoxin. The
CC protein has the toxic properties of the delta-endotoxin. Appln. is
CC at 0.2-10 x 1,000,000,000 I.U./acre.
XX
SQ Sequence 1178 AA;

Query Match 49.4%; Score 39; DB 7; Length 1178;
Best Local Similarity 45.5%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPASEHTH 14
II I : ::II
Db 432 pndptvndyth 442

Search completed: February 2, 2001, 10:38:03
Job time: 136 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:41:50 ; Search time 20.39 Seconds

(without alignments)
23.757 Million cell updates/sec

Title: US-09-273-217-4

Perfect score: 78

Sequence: 1 FAHADPTSGFSSIP 15

Scoring table: BIOSUM62

Gap: 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

88757

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	523	1	PI22001 homo sapien
2	71	91.0	523	1	PI5384 rattus norv
3	71	91.0	528	1	PI6390 mus musculu
4	59	75.6	653	1	PI22459 homo sapien
5	59	75.6	654	1	O61423 mus musculu
6	59	75.6	654	1	Q28527 mustela put
7	59	75.6	655	1	PI5385 rattus norv
8	59	75.6	660	1	Q05037 bos taurus
9	49	62.8	529	1	PI7658 homo sapien
10	49	62.8	602	1	PI9024 rattus norv
11	48	61.5	495	1	Q09470 homo sapien
12	48	61.5	495	1	PI6388 mus musculu
13	48	61.5	495	1	PI4099 rattus norv
14	48	61.5	530	1	PI7659 rattus norv
15	48	61.5	601	1	P79197 mustela put
16	47	60.3	598	1	P50638 oryctolagus
17	47	60.3	613	1	PI22460 homo sapien
18	46	59.0	499	1	PI6389 mus musculu
19	46	59.0	499	1	PI5386 mus musculu
20	46	59.0	499	1	P22739 xenopus lae
21	45	57.7	415	1	P73368 homo sapien
22	44	56.4	602	1	O61762 mus musculu
23	43	55.1	597	1	P10122 bos taurus
24	42	53.8	334	1	P10182 herpes simp
25	42	53.8	802	1	O63099 rattus norv
26	42	53.8	806	1	O62953 homo sapien
27	41	52.6	78	1	PI6511 conus texti
28	41	52.6	414	1	O62762 rattus norv
29	41	52.6	575	1	Q08101 bovine herp
30	40	51.3	273	1	Q09081 oryctolagus
31	40	51.3	330	1	O39940 bacillus su
32	40	51.3	446	1	Q12239 bombyx mori
33	40	51.3	742	1	PI5835 homo sapien

ALIGNMENTS

34	40	51.3	853	1	CIK3_RAT	PI5387 rattus norv
35	40	51.3	854	1	CIK3_HUMAN	Q14721 homo sapien
36	39	50.0	268	1	VF62_BPML5	Q05273 mycobacteri
37	39	50.0	407	1	FTS2_STRGR	P45501 streptomyc
38	39	50.0	447	1	KC13_HUMAN	O9y6m4 homo sapien
39	39	50.0	448	1	KC13_RAT	O62763 rattus norv
40	39	50.0	612	1	BA1_RAT	P07882 rattus norv
41	39	50.0	616	1	CIK1_DROME	P08510 drosophila
42	39	50.0	643	1	CIK2_DROME	P08511 drosophila
43	39	50.0	656	1	CIK4_DROME	P08513 drosophila
44	38	48.7	386	1	P53_FELCA	P41685 felis silve
45	38	48.7	507	1	DNA_MYCTU	P49993 mycobacteri

RESULT 1

CIK3_HUMAN	STANDARD:	PRT:	523 AA.
AC	PI22001:		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HGK5) (HUKIII) (HLK3).		
GN	KCNK3 OR HGK5.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=SKELTAL MUSCLE;		
RX	MEDLINE=91095456; PubMed=1986382;		
RA	Phillipson L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I., Nelson D.J., Steiner D.F.;		
RT	*Sequence and functional expression in Xenopus oocytes of a human insulinoma and islet potassium channel.*;		
RT	Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=LYMPHOCYTES;		
RC	MEDLINE=92189730; PubMed=1547020;		
RX	Cai Y.-C., Osborne P.B., North R.A., Dooley D.C., Douglas J., Lesage F., Ricard P., Barhanin J., Lazdunski M.;		
RT	*Characterization and functional expression of genomic DNA encoding the human lymphocyte type n potassium channel.*;		
RT	DNA Cell Biol. 11:163-172(1992).		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=92235098; PubMed=1373731;		
RX	Attali B., Romey G., Honore E., Schmid-Alliana A., Mattel M.-G., Lesage F., Ricard P., Barhanin J., Lazdunski M.;		
RT	*Cloning, functional expression, and regulation of two K+ channels in human T lymphocytes.*;		
RT	J. Biol. Chem. 267:8650-8657(1992).		
RL	[4]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=BL00D;		
RX	MEDLINE=95130104; PubMed=7829094;		
RA	Folander K., Douglas J., Swanson R.;		
RT	*Confirmation of the assignment of the gene encoding Kv1.3, a voltage-gated potassium channel (KCNK3) to the proximal short arm of human chromosome 1.*;		
RT	Genomics 23:295-296(1994).		
RL	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.		
CC	-I- SUBUNIT: HETEROPTRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).		
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE		

CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M55515; AAA36425.1; -
 CC EMBL: M38217; AAB88073.1; -
 CC EMBL: M85217; AAA59457.1; -
 CC EMBL: L23499; AAC31761.1; -
 CC HSSP: P03621; 2IFN.
 CC MIM: 176263; -
 CC INTERPRO: IPR000636; -
 CC INTERPRO: IPR003091; -
 CC PRAM: PF00520; Ion_trans; 1.
 CC PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC FT TRANSMEM 183 201 SEGMENT S1.
 CC FT TRANSMEM 243 264 SEGMENT S2.
 CC FT TRANSMEM 276 296 SEGMENT S3.
 CC FT TRANSMEM 311 329 SEGMENT S4.
 CC FT TRANSMEM 346 365 SEGMENT S5.
 CC FT TRANSMEM 407 429 SEGMENT S6.
 CC FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 227 227 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT MOD_RES 468 468 PHOSPHORYLATION (BY CARK)
 CC FT MOD_RES 468 468 (POTENTIAL).
 CC FT CONFLICT 20 20 A -> G (IN REF. 1).
 CC FT CONFLICT 37 37 L -> V (IN REF. 1).
 CC FT CONFLICT 61 61 L -> V (IN REF. 3).
 CC FT CONFLICT 91 91 L -> V (IN REF. 1).
 CC FT CONFLICT 257 257 E -> K (IN REF. 4).
 CC FT CONFLICT 338 338 T -> S (IN REF. 1).
 CC FT CONFLICT 419 419 T -> S (IN REF. 1).
 CC FT CONFLICT 488 488 S -> T (IN REF. 1).
 CC SO SEQUENCE 523 AA; 58303 MW; 8BA2F1C7C802BA11 CRC64;

Query Match 100.0%; Score 78; DB 1; Length 523;
 Best local Similarity 100.0%; Pred. No. 6; 7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FARADPTSGFSSIP 15
 DB 366 FARADPTSGFSSIP 380

RESULT 2
 C1K3_RAT STANDARD; PRT; 525 AA.
 AC P15384;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (RGK5) (RK33) (KV3).
 GN KCNA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;
 RX MEDLINE-90059914; Pubmed-2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain."
 RL EMBO J. 8:3235-3244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-90297965; Pubmed-2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Foldenauer K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT "Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain."
 RL Neuron 4:929-939(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPHOCYTES;
 RX MEDLINE-90278098; Pubmed-2351830;
 RA Douglass J., Osborne P.B., Cai Y.C., Wilkinson M., Christie M.J.,
 RA Adelman J.P.;
 RT "Characterization and functional expression of a rat genomic DNA
 RT clone encoding a lymphocyte potassium channel."
 RL J. Immunol. 144:4841-4850(1990).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X16001; CAA34132.1; -
 CC EMBL: M30312; AAA42035.1; -
 CC EMBL: M31744; AAA41500.1; -
 CC PIR: S06708; S06708.
 CC PIR: JH0168; JH0168.
 CC HSSP: P03621; 2IFN.
 CC DR INTERPRO: IPR000636; -
 CC DR INTERPRO: IPR003091; -
 CC PRAM: PF00520; Ion_trans; 1.
 CC PRINTS: PR00169; KCHANNEL.
 CC KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Multigene family; Phosphorylation.
 CC FT TRANSMEM 185 203 SEGMENT S1.
 CC FT TRANSMEM 245 266 SEGMENT S2.
 CC FT TRANSMEM 278 298 SEGMENT S3.
 CC FT TRANSMEM 313 331 SEGMENT S4.
 CC FT TRANSMEM 348 367 SEGMENT S5.
 CC FT TRANSMEM 409 431 SEGMENT S6.
 CC FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT MOD_RES 470 470 PHOSPHORYLATION (BY CAPK)
FT CONFLICT 106 106 F -> L (IN REF. 1).
FT CONFLICT 181 181 G -> R (IN REF. 3).
FT CONFLICT 430 430 V -> L (IN REF. 3).
SQ SEQUENCE 525 AA: 58424 MW: 6DA869D5471C401 CRC64:

Query Match 91.0%; Score 71; DB 1; Length 525;
Best Local Similarity 86.7%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPGSGFSSIP 15
Db 368 FAADDPGSGFSSIP 382

RESULT 3
CIRK_MOUSE STANDARD: PRT: 528 AA.
AC P16390.
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.3 (MK3).
GN KCNA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-90161996; PubMed-2305265;
RA Chandry K.G., Williams C.B., Spencer R.H., Aguilar B.A.,
RA Ghanshani S., Tempel B.L., Guitman G.A.;
RT "A family of three mouse potassium channel genes with intronless
RT coding regions."
RT Science 247:973-975(1990).
RL
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATION IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M30441; AAA39716.1; -.
CC HSSP: P03621; 2IFN.
CC MGS: MGI:96660; KCNA3.
CC INTERPRO: IPR000636; -.
CC INTERPRO: IPR003091; -.
CC PFM: PF00520; Ion_trans. 1.
CC PRINTS: PR00169; KCHANNEL.
CC Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
CC Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 188 206 SEGMENT S1.
```

```
FT TRANSMEM 248 269 SEGMENT S2.
FT TRANSMEM 281 301 SEGMENT S3.
FT TRANSMEM 316 334 SEGMENT S4.
FT TRANSMEM 351 370 SEGMENT S5.
FT TRANSMEM 412 434 SEGMENT S6.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 473 473 PHOSPHORYLATION (BY CAPK)
SQ SEQUENCE 528 AA: 58526 MW: CBD65F1515F9A731 CRC64:

Query Match 91.0%; Score 71; DB 1; Length 528;
Best Local Similarity 86.7%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPGSGFSSIP 15
Db 371 FAADDPGSGFSSIP 385

RESULT 4
CIRK_HUMAN STANDARD: PRT: 653 AA.
AC P22459.
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.4 (HK1) (HPCN2) (HBK4)
DE (HUK11).
GN KCNA4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-SKELETAL MUSCLE;
RA MEDLINE-91095456; PubMed-1986382;
RA Philipson L.H., Hice R.E., Schaefer K., Lamendola J., Bell G.I.,
RA Nelson D.J., Steiner D.F.;
RT "Sequence and functional expression in Xenopus oocytes of a human
RT insulinoma and islet potassium channel."
RT Proc. Natl. Acad. Sci. U.S.A. 88:53-57(1991).
RL
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE-SKELETAL MUSCLE;
RA MEDLINE-91088321; PubMed-2263489;
RA Philipson L.H., Schaefer K., Lamendola J., Bell G.I., Steiner D.F.;
RT "Sequence of a human fetal skeletal muscle potassium channel cDNA
RT related to RCK4."
RT Nucleic Acids Res. 18:7160-7160(1990).
RL
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE-HEART;
RA MEDLINE-91160866; PubMed-2001794;
RA Tamkun M.M., Kloth K.M., Walbridge J.A., Kroemer H., Roden D.M.,
RA Glover D.M.;
RT "Molecular cloning and characterization of two voltage-gated K+
RT channel cDNAs from human ventricle."
RT FASEB J. 5:331-337(1991).
RL
RN [4]
RP SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RA Ramaswami M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RA Mathew M.K.;
RT "Human potassium channel genes: molecular cloning and functional
RT expression."
RT Mol. Cell. Neurosci. 1:214-223(1990).
RL
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
```

CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M55514; AAA60034.1; -;
 DR EMBL: M60450; AAA61275.1; -;
 DR EMBL: L02751; AAA36140.1; -;
 DR PIR: S12630; S12630.
 DR HSSP: P15385; 1ZTO.
 DR MIM: 176266; -;
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR003091; -;
 DR PRAM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KM Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSSEM 308 326 SEGMENT S1 (POTENTIAL).
 FT TRANSSEM 371 392 SEGMENT S2 (POTENTIAL).
 FT TRANSSEM 404 424 SEGMENT S3 (POTENTIAL).
 FT TRANSSEM 443 461 SEGMENT S4 (POTENTIAL).
 FT TRANSSEM 478 497 SEGMENT S5 (POTENTIAL).
 FT TRANSSEM 539 561 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 62 65 POLY-HIS.
 FT DOMAIN 123 137 POLY-GLU.
 FT DOMAIN 162 165 POLY-GLY.
 FT DOMAIN 433 436 POLY-GLN.
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 90 90 PHOSPHORYLATION (BY CAPE).
 FT MOD_RES 90 90 (POTENTIAL).
 FT MOD_RES 599 599 PHOSPHORYLATION (BY CAPE).
 FT MOD_RES 599 599 (POTENTIAL).
 FT CONFLICT 38 38 R -> A (IN REF. 3 AND 4).
 FT CONFLICT 42 42 R -> A (IN REF. 3 AND 4).
 FT CONFLICT 84 88 EEEAT -> RRRRO (IN REF. 3 AND 4).
 FT CONFLICT 304 304 D -> S (IN REF. 3 AND 4).
 FT CONFLICT 542 542 V -> S (IN REF. 3 AND 4).
 FT CONFLICT 631 631 A -> G (IN REF. 3 AND 4).
 SQ SEQUENCE 653 AA; 73288 MW; 7A66781B87D6F27 CRC64;

Query Match 75.6%; Score 59; DB 1; Length 653;
 Best Local Similarity 73.3%; Pred. No. 0.015; Mismatches 2; Indels 0; Gaps 0;
 Matches 11; Conservative 2;

QY 1 FAADPTGSPSSIP 15
 |||||:|:|:|
 Db 498 FAADPTGSPSSIP 512

RESULT 5
 CIR4_MOUSE STANDARD; PRT; 654 AA.
 ID 061423;
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL4.
 GN KCNA4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AKR;
 RX MEDLINE-94297198; PubMed-8020965;
 RA Wymore R.S., Kosenberg J.R., Kinoshita K.D., Aiyer J., Coyne C.,
 RA Chen X.N., Hustad C.M., Copeland N.G., Gutman G.A., Jenkins N.A.,
 RA Chandy K.G.;
 RT "Genomic organization, nucleotide sequence, biophysical properties,
 RT and localization of the voltage-gated K+ channel gene KCNA4/Kv1.4 to
 RT mouse chromosome 2/human 11p14 and mapping of KCNC1/Kv3.1 to mouse
 RT 7/human 11p14.3-p15.2 and KCNA1/Kv1.1 to human 12p13."
 RL Genomics 20:191-202(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U03723; AAB60668.1; -;
 DR HSSP: P15385; 1ZTO.
 DR MED: MGI:96661; KCNA4.
 DR INTERPRO: IPR000636; -;
 DR INTERPRO: IPR003091; -;
 DR PRAM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
 FT TRANSSEM 309 327 SEGMENT S1 (POTENTIAL).
 FT TRANSSEM 372 393 SEGMENT S2 (POTENTIAL).
 FT TRANSSEM 405 425 SEGMENT S3 (POTENTIAL).
 FT TRANSSEM 444 462 SEGMENT S4 (POTENTIAL).
 FT TRANSSEM 479 498 SEGMENT S5 (POTENTIAL).
 FT TRANSSEM 540 562 SEGMENT S6 (POTENTIAL).
 FT DOMAIN 38 50 POLY-ALA.
 FT DOMAIN 62 65 POLY-HIS.
 FT DOMAIN 83 89 POLY-ARG.
 FT DOMAIN 123 137 POLY-GLU.
 FT DOMAIN 162 166 POLY-GLY.
 FT DOMAIN 434 437 POLY-GLN.
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 643 643 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 600 600 PHOSPHORYLATION (BY CAPE).
 SQ SEQUENCE 654 AA; 73473 MW; 8693651A30BD36D4 CRC64;

Query Match 75.6%; Score 59; DB 1; Length 654;
 Best Local Similarity 73.3%; Pred. No. 0.015;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAADPTSGFSSIP 15
 |||||:|:| |
 DB 499 FAADPTTHQOSIP 513

RESULT 6
 C1K4_MUSPF STANDARD: PRT: 654 AA.
 ID C1K4_MUSPF Q28527:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.4 (FK1).
 GN KCNA4.
 OS Muscula putorius furo (Perret).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustellidae; Mustela.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART VENTRICLE; PubMed=7943383;
 RX MEDLINE=95029958; PubMed=7943383;
 RA Comer M.B., Campbell D.L., Rasmusson R.L., Lanson D.R.,
 RA Morales M.J., Zhang Y., Strauss H.C.;
 RT "Cloning and characterization of an Ito-like potassium channel from
 RT ferret ventricle.";
 RL Am. J. Physiol. 267:H1383-H1395(1994).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. LEFT AND RIGHT
 CC VENTRICLE AND KIDNEY BUT NOT IN SKELETAL MUSCLE, ENDOTHELIAL
 CC CELLS, AORTA, AND LIVER.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -1- SIMILIARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
 CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U06156; AAB60261.1; -
 DR HSSP: P15385; I270.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFM: PF00520; Ion_trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KM Glycoprotein; Multigene family; Ion transport; Voltage-gated channel;
 FT TRASMEN 309 327
 FT TRASMEN 372 393
 FT TRASMEN 405 425
 FT TRASMEN 444 462
 FT TRASMEN 479 498
 FT TRASMEN 540 562
 SEGMENT S1 (POTENTIAL).
 SEGMENT S2 (POTENTIAL).
 SEGMENT S3 (POTENTIAL).
 SEGMENT S4 (POTENTIAL).
 SEGMENT S5 (POTENTIAL).
 SEGMENT S6 (POTENTIAL).

Query Match 75.6%; Score 59; DB 1; Length 654;
 Best Local Similarity 73.3%; Pred. No. 0.015;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 FAADPTSGFSSIP 15
 |||||:|:| |
 DB 499 FAADPTTHQOSIP 513

RESULT 7
 C1K4_RAT STANDARD: PRT: 655 AA.
 ID C1K4_RAT P15385:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.4 (RCK4) (RHK1) (RK4).
 GN KCNA4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN; PubMed=2555158;
 RX MEDLINE=90039914; PubMed=2555158;
 RA Stuehmer W., Ruppersberg J.P., Schroeter K.H., Sakmann B.,
 RA Stocker M., Giese K.P., Perschke A., Baumann A., Pongs O.;
 RT "Molecular basis of functional diversity of voltage-gated potassium
 RT channels in mammalian brain.";
 RL EMBO J. 8:3235-3244(1989).
 CC [2]
 CC SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=HEART;
 RX MEDLINE=90346174; PubMed=2384173;
 RA Tseng-Crank J., Tseng G.-N., Schwartz A., Tanouye M.A.;
 RT "Molecular cloning and functional expression of a potassium channel
 RT cDNA isolated from a rat cardiac library.";
 RL FEBS Lett. 268:63-68(1990).
 CC [3]
 CC STRUCTURE BY NMR OF 1-37.
 RX MEDLINE=97152495; PubMed=9000078;
 RA Antz C., Geyer M., Pakler B., Schott M.K., Guy H.R., Frank R.,
 RA Ruppersberg J.P., Kalbitzer H.R.;
 RT "NMR structure of inactivation gates from mammalian voltage-dependent
 RT potassium channels.";
 RL Nature 385:272-275(1997).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: HEART AND BRAIN.
 CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS

CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X16002; CA434133.1; -
CC DR EMBL: M32867; AAA41469.1; -
CC DR PIR: S06710; S06710.
CC DR PDB: 1ZTO; 05-JUN-97.
CC DR INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
CC DR PFAM: PF00520; Ion_trans; 1.
CC DR PRINTS: PR00169; KCHANNEL.
CC KW Glycophorin: Multigene family: Ion transport; Voltage-gated channel;
CC Ionic channel; Transmembrane; 3D-structure.
CC -----
CC TRANSMEM 310 328 SEGMENT S1 (POTENTIAL).
CC FT TRANSMEM 373 394 SEGMENT S2 (POTENTIAL).
CC FT TRANSMEM 406 426 SEGMENT S3 (POTENTIAL).
CC FT TRANSMEM 445 463 SEGMENT S4 (POTENTIAL).
CC FT TRANSMEM 480 499 SEGMENT S5 (POTENTIAL).
CC FT TRANSMEM 541 563 SEGMENT S6 (POTENTIAL).
CC FT DOMAIN 38 50 POLY-ALA.
CC FT DOMAIN 62 65 POLY-HIS.
CC FT DOMAIN 92 95 POLY-LYS.
CC FT DOMAIN 124 138 POLY-GLU.
CC FT DOMAIN 163 167 POLY-GLY.
CC FT DOMAIN 183 183 POLY-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 644 644 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT MOD_RES 601 601 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
CC FT CONFLICT 42 42 A -> L (IN REF. 2).
CC FT CONFLICT 84 88 EEEAT -> RRRRO (IN REF. 2).
CC FT CONFLICT 95 95 MISSING (IN REF. 2).
CC FT CONFLICT 310 310 G -> A (IN REF. 2).
CC SQ SEQUENCE 655 AA; 73390 MW; 40AEF2P901A05E43 CRC64;

Query Match 75.6%; Score 59; DB 1; Length 655;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
Db 500 FAEADPTTHFOSIP 514

RESULT 8
CIR4_BOVIN STANDARD; PRT; 660 AA.
ID CIR4_BOVIN
AC 005037;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL4 (BAK4).
GN KCNA4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENAL MEDULLA;
RX MEDLINE=92371645; PubMed=1505668;
RA Garcia-Guzman M., Calvo S., Cerna V., Criado M.;

RT "Molecular cloning and permanent expression in a neuroblastoma cell
RT line of a fast inactivating potassium channel from bovine adrenal
RT medulla".
RL FEBS Lett. 308:283-289(1992).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROETRAIMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE A-TYPE POTASSIUM
CC CURRENT CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X57033; CA40349.1; -
CC DR HSSP: P15385; 1ZTO.
CC DR INTERPRO: IPR000636; -
CC DR INTERPRO: IPR003091; -
CC DR PFAM: PF00520; Ion_trans; 1.
CC DR PRINTS: PR00169; KCHANNEL.
CC KW Glycophorin: Multigene family: Ion transport; Voltage-gated channel;
CC Ionic channel; Transmembrane; 3D-structure.
CC -----
CC TRANSMEM 316 334 SEGMENT S1 (POTENTIAL).
CC FT TRANSMEM 379 400 SEGMENT S2 (POTENTIAL).
CC FT TRANSMEM 412 432 SEGMENT S3 (POTENTIAL).
CC FT TRANSMEM 451 469 SEGMENT S4 (POTENTIAL).
CC FT TRANSMEM 486 505 SEGMENT S5 (POTENTIAL).
CC FT TRANSMEM 547 569 SEGMENT S6 (POTENTIAL).
CC FT DOMAIN 38 50 POLY-ALA.
CC FT DOMAIN 53 59 POLY-GLY.
CC FT DOMAIN 62 65 POLY-HIS.
CC FT DOMAIN 83 87 POLY-ARG.
CC FT DOMAIN 131 137 POLY-GLU.
CC FT DOMAIN 162 173 POLY-GLN.
CC FT DOMAIN 441 444 POLY-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 360 360 PHOSPHORYLATION (BY CAPK)
CC FT MOD_RES 607 607 (BY SIMILARITY).
CC SQ SEQUENCE 660 AA; 73512 MW; A1FAE59677929D5 CRC64;

Query Match 75.6%; Score 59; DB 1; Length 660;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
Db 506 FAEADPTTHFOSIP 520

RESULT 9
CIR6_HUMAN STANDARD; PRT; 529 AA.
ID CIR6_HUMAN
AC P17658;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.6 (HBRZ).
 GN KCNM6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RX MEDLINE-90269208; PubMed-2347305;
 RA Gruppe A., Schroeter K.H., Ruppersberg J.P., Stocker M., Drewes T.,
 RA Beckh S., Pongs O.;
 RT Cloning and expression of a human voltage-gated potassium channel. A
 RT novel member of the RCK potassium channel family.";
 RL EMBO J. 9:1749-1756(1990).
 CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -I- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
 CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
 CC COMPARTMENTS.
 CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X17622; CAA35623.1; -
 DR PIR: S15057; S15057.
 DR MIM: 176257; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFAM: PF00520; ion.trans.1.
 DR PRINTS: PR00169; KCHANNEL.
 DR KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 175 193 SEGMENT S1.
 FT TRANSMEM 263 284 SEGMENT S2.
 FT TRANSMEM 296 316 SEGMENT S3.
 FT TRANSMEM 340 360 SEGMENT S4.
 FT TRANSMEM 376 396 SEGMENT S5.
 FT TRANSMEM 437 457 SEGMENT S6.
 FT MOD_RES 511 511 PHOSPHORYLATION (BY CAPK)
 FT (PROBABLE).
 SO SEQUENCE 529 AA; 58728 MW; CFF0710A1F9C069F CRC64;

Query Match 62.8%; Score 49; DB 1; Length 529;
 Best Local Similarity 73.3%; Pred. No. 0.63;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.5 (KVL) (RCK7).
 GN KCNM5.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RX MEDLINE-90297965; PubMed-2361015;
 RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B.,
 RA Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A.,
 RA Bennett C., Stein R.B., Kaczmarek L.M.;
 RT Cloning and expression of cDNA and genomic clones encoding three
 RT delayed rectifier potassium channels in rat brain.";
 RL Neuron 4:929-939(1990).
 CC -I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -I- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -I- TISSUE SPECIFICITY: BRAIN.
 CC -I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
 CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -I- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
 CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
 CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
 CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
 CC -I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
 CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M27158; AAA41498.1; -
 DR PIR: JH0166; JH0166.
 DR HSSP: P03621; Z1EN.
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFAM: PF00520; ion.trans.1.
 DR PRINTS: PR00169; KCHANNEL.
 DR KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 242 260 SEGMENT S1.
 FT TRANSMEM 316 336 SEGMENT S2.
 FT TRANSMEM 347 368 SEGMENT S3.
 FT TRANSMEM 387 408 SEGMENT S4.
 FT TRANSMEM 423 444 SEGMENT S5.
 FT TRANSMEM 484 505 SEGMENT S6.
 FT DOMAIN 373 376 POLY-GLY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 44 44 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT MOD_RES 81 81 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 81 81 PHOSPHORYLATION (BY CR2) (POTENTIAL).
 FT MOD_RES 535 535 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 546 546 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 FT MOD_RES 569 569 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
 SO SEQUENCE 602 AA; 66552 MW; 6A784535FF226ED7 CRC64;

Query Match 62.8%; Score 49; DB 1; Length 602;


```

RL Nature 332:837-839(1988).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROPTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M30439; AAA39711.1; -.
DR EMBL: Y00305; CAA68408.1; -.
DR PIR: S06378; S06378.
DR PIR: A40090; A40090.
DR HSSP: P03621; 2IFN.
DR MGD: M61:96654; KCNA1.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PIR: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
DR KW Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycophorin; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 367 408 SEGMENT S6.
FT CAROHD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT FT PHOSPHORYLATION.
FT MOD_RES 446 446 PHOSPHORYLATION (BY CAPK)
FT FT (POTENTIAL).
SQ SEQUENCE 495 AA; 56409 MW; C9249F130E943D3D CRC64;

Query Match 61.5%; Score 48; DB 1; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15
DB 346 FAEAEAFESHSSIP 360

RESULT 13
CIRL_RAT
ID CIRL_RAT STANDARD: PRT; 495 AA.
AC P10499:
DT 01-APR-1990 (rel. 14, Created)
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (1A) (RBK1) (RCK1).
GN KCNA1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MEDLINE=89052659; PubMed=3191911;
RX Baumann A., Grupe A., Ackermann A., Pongs O.;
RT "Structure of the voltage-dependent potassium channel is highly
RT conserved from Drosophila to vertebrate central nervous systems.";
RL EMBL J. 7:2457-2463(1988).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=89203264; PubMed=2539643;
RA Christie M.J., Adelman J.P., Douglass J., North R.A.;
RT "Expression of a cloned rat brain potassium channel in Xenopus
RT oocytes.";
RL Science 244:221-224(1989).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROPTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12589; CAA31102.1; -.
DR EMBL: M26161; AAA1982.1; -.
DR PIR: A41353; A41353.
DR PIR: S01161; S01161.
DR HSSP: P03621; 2IFN.
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR003091; -.
DR PIR: PF00520; Ion.trans. 1.
DR PRINTS: PR00169; KCHANNEL.
DR KW Glycophorin; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycophorin; Multigene family; Phosphorylation.
FT TRANSMEM 168 186 SEGMENT S1.
FT TRANSMEM 221 242 SEGMENT S2.
FT TRANSMEM 254 274 SEGMENT S3.
FT TRANSMEM 290 309 SEGMENT S4.
FT TRANSMEM 326 345 SEGMENT S5.
FT TRANSMEM 367 408 SEGMENT S6.
FT CAROHD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 322 322 PHOSPHORYLATION (BY CAPK)
FT FT PHOSPHORYLATION.
FT MOD_RES 445 445 PHOSPHORYLATION (BY CAPK)
FT FT (POTENTIAL).
SQ SEQUENCE 495 AA; 56379 MW; 29804463133F5D31 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 495;
Best Local Similarity 66.7%; Pred. No. 0.87;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTSGFSSIP 15

```

Db 346 FAEAEASHPSIP 360

RESULT 14

CIRK6_RAT STANDARD; PRT; 530 AA.

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

GN KCNAG.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN CORTEX;

RX MEDLINE=90269208; Pubmed=2347305;

RA Grupe A., Schreuter K.H., Ruppersberg J.P., Stocker M., Drewes T., Beckh S., Pongs O.;

RT "Cloning and expression of a human voltage-gated potassium channel. A novel member of the RCK potassium channel family.";

RL EMBL J. 9:1749-1756(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=90297965; Pubmed=2361015;

RA Swanson R., Marshall J., Smith J., Williams J., Boyle M.B., Folander K., Luneau C.J., Antanavage J., Oliva C., Buhrow S.A., Bennett C., Stein R.B., Kaczmarek L.M.;

RT "Cloning and expression of cDNA and genomic clones encoding three delayed rectifier potassium channels in rat brain.";

RL Neuron 4:929-939(1990).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE=91130598; Pubmed=1993474;

RA Kirsch G.E., Drewe J.A., Verma S., Brown A.M., Joho R.H.;

RT "Electrophysiological characterization of a new member of the RCK family of rat brain K⁺ channels.";

RL FEBS Lett. 278:55-60(1991).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: BRAIN.

CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- MISCELLANEOUS: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: X17621; CA35622.1; -

DR EMBL; M21159; AAA41499.1; ALT_SEQ.

DR PIR; JH0167; JH0167.

DR PIR; S12786; S12786.

DR INTERPRO; IPR000636; -

DR INTERPRO; IPR003091; -

DR PFAM; PF00520; Ion_trans; 1.

DR PRINTS; PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Glycoprotein; Multigene family; Phosphorylation.

FT TRANSMEM 175 193 SEGMENT S1.

FT TRANSMEM 264 285 SEGMENT S2.

FT TRANSMEM 297 317 SEGMENT S3.

FT TRANSMEM 341 361 SEGMENT S4.

FT TRANSMEM 377 397 SEGMENT S5.

FT TRANSMEM 438 458 SEGMENT S6.

FT CARBOHYD 46 46

FT MOD_RES 222 222

FT MOD_RES 512 512

FT MOD_RES 528 528

FT MOD_RES 528 528

FT CONFLICT 241 241 S -> L (IN REF. 3).

FT CONFLICT 333 333 R -> G (IN REF. 2).

SQ SEQUENCE 530 AA; 58883 MW; 30A9774B66CF1DA5 CRC64;

Query Match 61.58; Score 48; DB 1; Length 530;

Best Local Similarity 73.38; Pred. No. 0.93;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 397 FAEADVDVSLPSIP 411

QY 1 FAEADPTGFSFIP 15

IIIIII I I I I I

RESULT 15

CIRK5_MUSPF STANDARD; PRT; 601 AA.

AC P79197;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5.

GN KCNA5.

OS Mus musculus furo (Ferret).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-HEART ATRIUM;

RA Schwiegel T., Folander K., Swanson R.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K⁺ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT (BY STIMULABILITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL: U45979; ABA41145.1; -
 DR INTERPRO: IPR000636; -
 DR INTERPRO: IPR003091; -
 DR PFWA: PF00520; Ion_Trans; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Glycoprotein; Multigene family; Phosphorylation.
 FT TRANSMEM 240 258 SEGMENT S1.
 FT TRANSMEM 314 334 SEGMENT S2.
 FT TRANSMEM 345 366 SEGMENT S3.
 FT TRANSMEM 386 407 SEGMENT S4.
 FT TRANSMEM 422 443 SEGMENT S5.
 FT TRANSMEM 483 504 SEGMENT S6.
 FT DOMAIN 370 375 POLY-GLY.
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 601 AA; 65889 MW; 142B9F8CB43FE0 CRC64;

Query Match 61.5%; Score 48; DB 1; Length 601;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 FAADDPTSGESSIP 15
 |||||: . |||||
 Db 442 FAADNQTTHSSIP 456

Search completed: February 2, 2001, 10:41:51
 Job time: 315 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:39:12 ; Search time 62.83 Seconds
(without alignments)
27.982 Million cell updates/sec

Title: US-09-273-217-4
Perfect score: 78
Sequence: 1 FAADDPSTGFSIP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	516	6 Q28656	Q28656 oryctolagus
2	74	94.9	27	13 Q73609	Q73609 gallus gall
3	73	93.6	136	6 Q09077	Q09077 sus scrofa
4	72	92.3	483	13 Q91829	Q91829 oncorhynch
5	56	71.8	27	13 Q73608	Q73608 gallus gall
6	56	71.8	494	13 Q91830	Q91830 oncorhynch
7	56	71.8	511	4 Q16322	Q16322 homo sapien
8	56	71.8	725	6 Q28649	Q28649 oryctolagus
9	54	69.2	662	13 Q9YXG8	Q9YXG8 gallus gall
10	50	64.1	602	11 Q9Z1R6	Q9Z1R6 mus musculu
11	48.5	62.2	543	10 Q9SBA8	Q9SBA8 arabisdopsis
12	48	61.5	529	11 Q61923	Q61923 mus musculu
13	48	61.5	593	6 Q28248	Q28248 canis famli
14	47	60.3	512	5 Q28597	Q28597 schistosoma
15	47	60.3	552	10 Q24019	Q24019 lycopersico
16	46	59.0	123	6 Q9NOE4	Q9NOE4 sus scrofa
17	46	59.0	141	6 Q09074	Q09074 sus scrofa
18	46	59.0	141	6 Q09075	Q09075 sus scrofa
19	46	59.0	460	5 Q09658	Q09658 caenorhabdi

ALIGNMENTS

Result ID	Query Match	Score	DB ID	Description
20	46	59.0	476	6 Q08635
21	46	59.0	490	5 Q9XXD1
22	46	59.0	499	6 Q28293
23	46	59.0	499	6 Q28293
24	45	57.7	273	6 Q9XSP9
25	45	57.7	433	10 Q9SUY9
26	45	57.7	489	13 Q91781
27	45	57.7	905	5 Q26344
28	44	56.4	330	2 Q9K987
29	43	55.1	2016	5 Q9VLS7
30	42	53.8	898	13 Q91592
31	42	53.8	908	5 Q18476
32	42	53.8	998	6 Q9N1D1
33	42	53.8	1104	3 Q9P553
34	41	52.6	41	4 Q9UD04
35	41	52.6	206	2 Q910X8
36	41	52.6	238	10 Q39962
37	41	52.6	422	5 Q9VEX2
38	41	52.6	488	5 Q25376
39	41	52.6	515	5 Q16968
40	41	52.6	575	12 Q65530
41	41	52.6	575	12 Q39506
42	41	52.6	575	12 Q9JE43
43	41	52.6	597	6 Q9FS07
44	41	52.6	834	2 Q9L1D0
45	41	52.6	2134	12 Q9YLS4

RESULT 1

Q28656 PRELIMINARY: PRT: 516 AA.

AC Q28656;
DT 01-NOV-1996 (TREMBLrel. 01. Created)
DI 01-NOV-1998 (TREMBLrel. 08. Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15. Last annotation update)
DE GILBENCILAMIDE-SENSITIVE VOLTAGE-GATED POTASSIUM CHANNEL.
GN KVL1.3-GLYB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE;
RX MEDLINE=96249424; PubMed=8647945;
RA Yao X., Chang A.Y., Boulpaep E.L., Segal A.S., Desir G.V.,
RT "Molecular cloning of a glibencilamide-sensitive, voltage-gated
RT potassium channel expressed in rabbit kidney."
RL J. Clin. Invest. 97:2525-2533(1996).
DR EMBL: U38240; AAC24718.1; -.
DR HSSP: 054397; 1B18
DR INTERPRO: IPR000636; -.
DR INTERPRO: IPR001622; -.
DR INTERPRO: IPR003091; -.
DR INTERPRO: IPR003131; -.
DR PFAM: PF00520; Ion.trans. 1.
DR PFAM: PF02214; K.tetra. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 516 AA; 57430 MW; 795E8498BCATCAAC CRC64;

Query Match 100.0%; Score 78; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. NO. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPSTGFSIP 15
DB 359 FAADDPSTGFSIP 373

```
RESULT 2
O73609 ID 073609 PRELIMINARY; PRT: 27 AA.
AC 073609:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE SHAKER-LIKE VOLTAGE-GATED POTASSIUM CHANNEL CKV1.1 (FRAGMENT).
GN CKV1.1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=COCHLEAR DUCT;
RX MEDLINE=98141813; PubMed=9473273;
RA Peale F.V., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain.";
RL Anal. Biochem. 256:158-168(1998).
DR EMBL: U62142; AAC06194.1; -.
KW Ionic channel.
FT NON_TER 1
FT TER 27
SQ SEQUENCE 27 AA; 2936 MW; 06BEFB440D5D9DD5 CRC64;

Query Match
Best Local Similarity 94.9%; Score 74; DB 13; Length 27;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
Db 4 FAADDPGSGSSIP 18

RESULT 3
O09077 ID 009077 PRELIMINARY; PRT: 136 AA.
AC 009077:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN (CLONE LLC3) (FRAGMENT).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92125505; PubMed=1733291;
RA Desit G.V., Hamlin H.A., Puente E., Reilly R.F., Hildebrandt F.,
RA Igarashi P.;
RT "Isolation of putative voltage-gated epithelial K-channel isoforms
RT from rabbit kidney and LLC-PK1 cells.";
RL Am. J. Physiol. 262:151-157(1992).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN RENAL EPITHELIAL TRANSPORT
CC AND MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF
CC MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO
CC THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A
CC POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN
CC ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: BELONGS TO THE SHAKER-RELATED POTASSIUM CHANNEL
CC SUBFAMILY 1.
DR HSSP: Q54397; 1BL8.
DR INTERPRO: IPR000636; -.
```

```
DR INTERPRO: IPR003091; -.
DR PFAM: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family.
FT NON_TER 1
FT TRANSMEM 1
FT TRANSMEM <1 6 SEGMENT S3.
FT TRANSMEM 22 39 SEGMENT S4.
FT TRANSMEM 56 75 SEGMENT S5.
FT TRANSMEM 116 136 SEGMENT S6.
FT NON_TER 136
SQ SEQUENCE 136 AA; 14827 MW; E8D95E192AA7FB97 CRC64;

Query Match
Best Local Similarity 93.6%; Score 73; DB 6; Length 136;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
Db 76 FREADDPGSGSSIP 90

RESULT 4
O91829 ID 091829 PRELIMINARY; PRT: 483 AA.
AC 091829:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE SHAKER-RELATED POTASSIUM CHANNEL TSHAZ.
OS Oncomorphus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE=98146169; PubMed=9486764;
RA Nguyen T.D., Jeserich G.;
RT "Molecular structure and expression of shaker type potassium channels
RT in glial cells of trout CNS.";
RL J. Neurosci. Res. 51:284-292(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Nguyen T.D., Jeserich G.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF252302; AAF70088.1; -.
KW Ionic channel.
SQ SEQUENCE 483 AA; 54955 MW; 68A78A8CA4424956 CRC64;

Query Match
Best Local Similarity 92.3%; Score 72; DB 13; Length 483;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 FAADDPGSGSSIP 15
Db 345 FAADDPGSGSSIP 359

RESULT 5
O73608 ID 073608 PRELIMINARY; PRT: 27 AA.
AC 073608:
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE SHAKER-LIKE VOLTAGE-GATED POTASSIUM CHANNEL CKV1.2 (FRAGMENT).
GN CKV1.2.
OS Gallus gallus (Chicken).
```


OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archaeosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WHITE LEGHORN; TISSUE=COCHLEAR DUCT;
 RX MEDLINE=98141813; PubMed=9473273;
 RA Peale F.V., Mason K., Hunter A.W., Bothwell M.;
 RT "Multimer display polymerase chain reaction amplifies and resolves
 RT related sequences sharing a single moderately conserved domain.";
 RL Anal. Biochem. 256:158-168(1998).
 DR EMBL: U62141; AAC06193.1; -.
 KW Ionic channel.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 27 AA; 3085 MW; EB081A9F65EAC123 CRC64;

 Query Match 71.8%; Score 56; DB 13; Length 27;
 Best Local Similarity 73.3%; Pred. No. 0.003;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 OY 1 FAEADPTSGFSSIP 15
 DB 4 FAEVDEPQSHFSSIP 18

 RESULT 6
 C91830
 ID 091830 PRELIMINARY; PRT; 494 AA.
 AC 091830.
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE SHAKER-RELATED POTASSIUM CHANNEL TSHAL.
 OS Oncohyunchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=98146169; PubMed=9486764;
 RA Nguyen T.D., Jeserich G.;
 RT "Molecular structure and expression of shaker type potassium channels
 RT in glial cells of trout CNS.";
 RL J. Neurosci. Res. 51:284-292(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Nguyen T.D., Jeserich G.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF252301; AAF70087.1; -.
 KW Ionic channel.
 SQ SEQUENCE 494 AA; 55899 MW; AF66998F97F22CD4 CRC64;

 Query Match 71.8%; Score 56; DB 13; Length 494;
 Best Local Similarity 73.3%; Pred. No. 0.071;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 OY 1 FAEADPTSGFSSIP 15
 DB 343 FAEVDEPQSHFSSIP 357

 RESULT 7
 Q16322
 ID Q16322 PRELIMINARY; PRT; 511 AA.
 AC Q16322;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CYCLIC GMP GATED POTASSIUM CHANNEL.
 GN KCNI OR C2-3A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97321042; PubMed=9177773;
 RA Orlas M., Bray-Ward P., Curran M.E., Keating M.T., Desir G.V.;
 RT "Genomic localization of the human gene for KCNA10, a cGMP-activated K
 RT channel.";
 RL Genomics 42:33-37(1997).
 RN [2]
 RP SEQUENCE OF 434-479 FROM N.A.
 RX MEDLINE=95309039; PubMed=7789190;
 RA Landes G.M., Curran M.E., Keating M.T.;
 RT "Molecular characterization and refined genomic localization of three
 RT human potassium ion channel genes.";
 RL Cytogenet. Cell Genet. 70:280-284(1995).
 DR EMBL: U96110; AAC51333.1; -.
 DR EMBL: S77547; AAB34663.1; -.
 DR HSSP: Q54397; IBL8.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR001622; -.
 DR INTERPRO: IPR003091; -.
 DR INTERPRO: IPR003131; -.
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 511 AA; 57784 MW; 1B09B1CD68745F29 CRC64;

 Query Match 71.8%; Score 56; DB 4; Length 511;
 Best Local Similarity 73.3%; Pred. No. 0.074;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 OY 1 FAEADPTSGFSSIP 15
 DB 395 FAEVDEPQSHFSSIP 409

 RESULT 8
 Q28649
 ID 028649 PRELIMINARY; PRT; 725 AA.
 AC 028649.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CGMP-GATED POTASSIUM CHANNEL.
 GN KCNI.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NEW ZEALAND WHITE;
 RX MEDLINE=96102184; PubMed=8524834;
 RA Yao X., Segal A.S., Welling P., Zhang X., McNicholas C.M., Engel D.,
 RA Boupaep E.L., Desir G.V.;
 RT "Primary structure and functional expression of a cGMP-gated potassium
 RT channel.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11711-11715(1995).
 DR EMBL: U38182; AAA92054.1; -.
 DR HSSP: Q54397; IBL8.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR001622; -.
 DR INTERPRO: IPR003091; -.
 DR INTERPRO: IPR003131; -.

DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic Channel.
 SQ SEQUENCE 725 AA; 80964 MW; 09C538F7BF4EDBD CRC64;

Query Match 71.88; Score 56; DB 6; Length 725;
 Best Local Similarity 73.38; Pred. No. 0.11;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 609 FAEVDEPESHSSIP 623

RESULT 9
 O9YX8 PRELIMINARY; PRT: 662 AA.
 AC O9YX8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE POTASSIUM CHANNEL SHAKER CKV1.4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9197209; PubMed-10095080;
 RA Rajeevan M.S., Hu S., Sakai Y., Sokolowski B.H.A.;
 RT "Cloning and expression of Shaker alpha- and beta-subunits during
 RT inner ear development.";
 RL Brain Res. Mol. Brain Res. 66:83-93(1999).
 DR EMBL: U82365; AAD1454.1; -.
 DR HSSP: P13385; 1270.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR001622; -.
 DR INTERPRO: IPR003091; -.
 DR INTERPRO: IPR003131; -.
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic Channel.
 SQ SEQUENCE 662 AA; 74061 MW; 7DB994240DF58007 CRC64;

Query Match 69.28; Score 54; DB 13; Length 662;
 Best Local Similarity 66.78; Pred. No. 0.22;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 507 FAEADPTSGFSSIP 521

RESULT 10
 O9ZIR6 PRELIMINARY; PRT: 602 AA.
 AC O9ZIR6;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VENTRICULAR POTASSIUM CHANNEL KV1.5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka H., Janzen K., Winkfein R.J., Fiset C., Clark B., Giles W.R.;

RT "Cloning and functional expression of mouse heart K+ channel alpha-
 RT subunits, Kv1.5, Kv4.2, and Kv4.3.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF108659; AAD13779.1; -.
 DR HSSP: Q54397; 1BL8.
 DR INTERPRO: IPR000636; -.
 DR INTERPRO: IPR001622; -.
 DR INTERPRO: IPR003091; -.
 DR INTERPRO: IPR003131; -.
 DR PFAM: PF00520; Ion_trans; 1.
 DR PFAM: PF02214; K_tetra; 1.
 DR PRINTS: PR00169; KCHANNEL.
 KW Ionic Channel.
 SQ SEQUENCE 602 AA; 66579 MW; 02926E85DC022DDA CRC64;

Query Match 64.18; Score 50; DB 11; Length 602;
 Best Local Similarity 73.38; Pred. No. 1;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 443 FAEADNGSHSSIP 457

RESULT 11
 O9SBA8 PRELIMINARY; PRT: 543 AA.
 ID O9SBA8;
 AC O9SBA8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE GTP CYCLOHYDROLASE II / 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE.
 GN RIBA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Herz S.W., Eberhardt S., Bacher A.;
 RT "Biosynthesis of riboflavin in plants. The riba gene of Arabidopsis
 RT thaliana specifies a bifunctional GTP cyclohydrolase II/3,4-
 RT dihydroxy-2butanone-4-phosphate synthase.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1000053; CA03884.1; -.
 DR INTERPRO: IPR000422; -.
 DR INTERPRO: IPR000926; -.
 DR PFAM: PF00925; GTP_cyclohydrol2; 1.
 DR PFAM: PF00926; DHBP_synthase; 1.
 KW Hydrolase.
 SQ SEQUENCE 543 AA; 59055 MW; 31DB9A500E42BF81 CRC64;

Query Match 62.28; Score 48.5; DB 10; Length 543;
 Best Local Similarity 63.28; Pred. No. 1.7;
 Matches 12; Conservative 0; Mismatches 2; Indels 5; Gaps 1;
 OY 2 AEADD-----PTSGFSSIP 15
 |||||:|||||

Db 114 AEDDFELDLPTGFSIP 132

RESULT 12
 ID O61923 PRELIMINARY; PRT: 529 AA.
 AC O61923;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE MORINE POTASSIUM CHANNEL PROTEIN.
 GN MK1.6.

```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mignon M.B., Street V.A., Demas V.P., Tempel B.L.;
RL Epilepsy Res. 0:0-0(0);
DR EMBL; M96688; AAA39772.1; -
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR003091; -
DR INTERPRO; IPR003131; -
DR PFAM; PF00520; ion_trans. 1.
DR PFAM; PF02214; K_tetra. 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel.
SQ SEQUENCE 529 AA; 58673 MW; 336D78C069ABEADD CRC64;

Query Match
Best Local Similarity 61.5%; Score 48; DB 11; Length 529;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAADDPGSGFSSIP 15
DB 396 FAADDPVDSLPSIP 410

RESULT 13
O28248 PRELIMINARY; PRT; 593 AA.
AC O28248;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE DELAYED RECTIFIER K+ CHANNEL (FRAGMENT).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON.
RA Overturn K.E., Russell S.N., Carl A., Vogalis R., Hart P.J.,
RA Hume J.R., Sanders K.M., Horowitz B.;
RL Am. J. Physiol. 267:0-0(1994).
DR EMBL; U08596; AAA57320.1; -
DR HSSP; 054397; 1BL8.
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR003091; -
DR INTERPRO; IPR003131; -
DR PFAM; PF00520; ion_trans. 1.
DR PFAM; PF02214; K_tetra. 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel.
FT NON_TER 593
SQ SEQUENCE 593 AA; 65617 MW; 056278731409B228 CRC64;

Query Match
Best Local Similarity 61.5%; Score 48; DB 6; Length 593;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAADDPGSGFSSIP 15
DB 435 FAADNQHETHFSSIP 449

RESULT 14
O26597 PRELIMINARY; PRT; 512 AA.
ID O26597
```

```
AC O26597;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE POTASSIUM CHANNEL PROTEIN.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;
OC Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95191947; PubMed=7533899;
RA Kim E., Day T.A., Bennett J.L., Pax R.A.;
RT "Cloning and functional expression of a Shaker-related voltage-gated
RT potassium channel gene from Schistosoma mansoni (Trematoda:
RT Digenea)."
RT Parasitology 110:171-180(1995).
DR EMBL; I26968; AAC37227.1; -
DR INTERPRO; IPR000636; -
DR INTERPRO; IPR001622; -
DR INTERPRO; IPR003091; -
DR INTERPRO; IPR003131; -
DR PFAM; PF00520; ion_trans. 1.
DR PFAM; PF02214; K_tetra. 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 512 AA; 58602 MW; 265DB2BA31742D39 CRC64;

Query Match
Best Local Similarity 60.3%; Score 47; DB 5; Length 512;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAADDPGSGFSSIP 15
DB 361 FAADADTSLFSSIP 375

RESULT 15
O24019 PRELIMINARY; PRT; 552 AA.
ID O24019;
AC O24019;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE GTP CYCLOHYDROLASE II/ 3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE.
GN RIBA.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UC82B;
RA Herz S.W., Eberhardt S., Bacher A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ002298; CAA05308.1; -
DR INTERPRO; IPR000422; -
DR INTERPRO; IPR000926; -
DR PFAM; PF00925; GTP_cyclohydro2. 1.
DR PFAM; PF00926; DHP_synthase. 1.
DR PRODOM; PD003034; -; 1.
KW Hydrolase.
SQ SEQUENCE 552 AA; 59750 MW; C14686752533325D CRC64;

Query Match
Best Local Similarity 60.3%; Score 47; DB 10; Length 552;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 EADDPGSGFSSIP 15
```

Db : | | | | | | | | | |
120 DLRPEGFSSVP 132

Search completed: February 2, 2001, 10:39:13
Job time: 202 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:37:13 ; Search time 38.22 Seconds
(without alignments)
26.649 Million cell updates/sec

Title: US-09-273-217-4
Perfect score: 78
Sequence: 1 FAEDDPTSGFSSIP 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	523	2 A38101	potassium channel
2	78	100.0	523	2 I52990	voltage-gated pota
3	71	91.0	57	2 S09044	potassium channel
4	71	91.0	525	2 A43531	potassium channel
5	71	91.0	528	2 I84205	potassium channel
6	63	80.8	57	2 S09045	potassium channel
7	59	75.6	653	2 A39922	potassium channel
8	59	75.6	654	2 S11049	potassium channel
9	59	75.6	654	2 E39113	potassium channel
10	59	75.6	660	2 S24125	potassium channel
11	50	64.1	49	2 S09049	potassium channel
12	49	62.8	529	2 S12787	potassium channel
13	49	62.8	602	2 JH0166	potassium voltage-
14	48	61.5	57	2 S09042	potassium channel
15	48	61.5	57	2 S09043	potassium channel
16	48	61.5	495	2 I57680	potassium channel
17	48	61.5	495	2 A40090	potassium channel
18	48	61.5	495	2 B39113	potassium channel
19	48	61.5	530	2 JH0167	potassium channel
20	47	60.3	552	2 T06410	GTP cyclohydrolase
21	47	60.3	598	2 S66669	potassium channel
22	47	60.3	613	2 A56031	potassium channel
23	46	59.0	57	2 S09046	potassium channel
24	46	59.0	460	2 T27759	hypothetical prote
25	46	59.0	476	2 S21144	potassium channel
26	46	59.0	490	2 T26983	hypothetical prote
27	46	59.0	499	2 JH0313	potassium channel
28	46	59.0	499	2 I77466	potassium channel
29	46	59.0	499	2 A48672	delayed rectifier

30	46	59.0	499	2 I84204	potassium channel
31	46	59.0	489	2 A33814	potassium channel
32	45	57.7	499	2 I51532	potassium channel
33	44	56.4	514	2 C49507	potassium channel
34	44	56.4	602	2 A49507	potassium channel
35	43	55.1	597	2 A33668	sterol esterase (E
36	42	53.8	334	1 DGBEX2	uracil-DNA glycosy
37	42	53.8	802	2 JH0595	potassium channel
38	42	53.8	1104	2 T49647	MSP1 related prote
39	41	52.6	78	2 S12513	delta-conotoxin tx
40	41	52.6	238	2 T10760	citrate-binding pr
41	41	52.6	414	2 B56711	casein kinase I (E
42	41	52.6	575	2 S35786	glycoprotein 9E -
43	41	52.6	597	2 S51212	BAK5 protein - bov
44	40	51.3	330	2 C69593	3-methyl-2-oxobuta
45	40	51.3	357	2 T09261	JUN kinase-activat

ALIGNMENTS

```

RESULT 1
A38101
potassium channel KCNA3 - human
N:Alternate names: potassium channel HUK3; potassium channel PCN3; shaker-related pot
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-1999
C:Accession: A38101; B38556
R:Attali, B.; Romey, G.; Honore, E.; Schmid-Alliana, A.; Mattei, M.G.; Lesage, F.; Ri
J Biol Chem 267: 8650-8657, 1992
A:Title: Cloning, functional expression, and regulation of two K(+) channels in human
A:Reference number: A38101; MUID:92235098
A:Accession: A38101
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-523 <ATT>
A:Cross-references: GB:M55217; NID:g186664; PIDD:AAA59457.1; PID:g186665
R:Phillipson, L.H.; Hite, R.E.; Schaefer, K.; Lakendola, J.; Bell, G.I.; Nelson, D.J.;
Proc Natl Acad Sci U.S.A. 88, 53-57, 1991
A:Title: Sequence and functional expression in Xenopus oocytes of a human insulinoma
A:Reference number: A38556; MUID:91095456
A:Accession: B38556
A:Molecule type: DNA
A:Residues: 1-19, 'G', 21-36, 'V', 38-60, 'L', 62-90, 'V', 92-337, 'S', 339-418, 'S', 420-457, 'LS
A:Cross-references: GB:M55515
A:Gene: GDB: KCNA3
A:Cross-references: GDB:J28079; OMIM:176263
A:Map position: 1p21-1p13.3
C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; v

Query Match 100.0%; Score 78; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FAEDDPTSGFSSIP 15
Db 366 FAEDDPTSGFSSIP 380

RESULT 2
I52990
voltage-gated potassium channel - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52990
R:Gail, Y.C.; Osborne, P.B.; North, R.A.; Dooley, D.C.; Douglass, J.
DNA Cell Biol 11, 163-172, 1992
A:Title: Characterization and functional expression of genomic DNA encoding the human
A:Reference number: I52990; MUID:92189730
A:Accession: I52990
A:Status: preliminary; translated from GB/EMBL/DBJ

```

A:Molecule type: DNA
A:Residues: 1-523 <RNS>
A:Cross-references: GB:M38217; NID:g186670; PIDN:AA88073.1; PID:g186671
C:Genetics:
A:Gene: HGK5

Query Match 100.0%; Score 78; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 5,7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 FAEADDPPTSGFSSIP 15
|||||

Db 366 FAEADDPPTSGFSSIP 380

RESULT 3
S09044
potassium channel protein MK-3 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09044
R:Betscholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, P.O.
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis by
A:Reference number: S09042; MUID:90235950
A:Accession: S09044
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match 91.0%; Score 71; DB 2; Length 57;
Best Local Similarity 86.7%; Pred. No. 7,4e-06;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 FAEADDPPTSGFSSIP 15
|||||

Db 11 FAEADDPSSGFNSIP 25

RESULT 4
A43531
potassium channel Kv1.3 - rat
N:Alternate names: potassium channel Kv3; potassium channel RCK3; potassium channel RCK5
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 05-Nov-1999
C:Accession: A43531; JH0168; S06708
R:Douglas, J.; Osborne, P.B.; Cai, Y.C.; Wilkinson, M.; Christie, M.J.; Adelman, J.P.
J. Immunol. 144, 4841-4850, 1990
A:Title: Characterization and functional expression of a rat genomic DNA clone encoding
A:Reference number: A43531; MUID:90278098
A:Accession: A43531
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-525 <DOU>
R:Swanson, R.; Marshall, J.; Smith, J.S.; Williams, J.B.; Boyle, M.B.; Folander, K.; Lunt
Neuron 4, 929-939, 1990
A:Title: Cloning and expression of cDNA and genomic clones encoding three delayed rectifi
A:Reference number: JH0166; MUID:90297965
A:Accession: JH0168
A:Molecule type: DNA
A:Residues: 1-180, 'G', 182-525 <SMA>
A:Cross-references: GB:M31744; NID:g205104; PIDN:AAA1500.1; PID:g205105
A:Experimental source: brain
A>Note: only a list of differences from sequence S06708 is given
R:Stuenkel, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese, K.H.
EMBO J. 8, 3235-3244, 1989
A:Title: Molecular basis of functional diversity of voltage-gated potassium channels in
A:Reference number: S06708; MUID:90059914
A:Accession: S06708
A:Molecule type: mRNA

A:Residues: 1-105, 'L', 107-180, 'G', 182-525 <STU>
A:Cross-references: EMBL:X16001; NID:g57034; PIDN:CAA34132.1; PID:g57035
C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane
F:185-203/Domain: transmembrane #status predicted <TM1>
F:245-266/Domain: transmembrane #status predicted <TM2>
F:278-298/Domain: transmembrane #status predicted <TM3>
F:313-331/Domain: transmembrane #status predicted <TM4>
F:348-367/Domain: transmembrane #status predicted <TM5>
F:383-392/Domain: transmembrane beta strand #status predicted <TM6>
F:393-401/Domain: transmembrane beta strand #status predicted <TM7>
F:409-431/Domain: transmembrane #status predicted <TM8>
F:470/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 91.0%; Score 71; DB 2; Length 525;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 FAEADDPPTSGFSSIP 15
|||||

Db 368 FAEADDPSSGFNSIP 382

RESULT 5
I84205
potassium channel protein MK3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: C40090; I84205
R:Chandy, K.G.; Williams, C.B.; Spencer, R.H.; Aguilar, B.A.; Ghanahani, S.; Tempel,
Science 247, 973-975, 1990
A:Title: A family of three mouse potassium channel genes with intronless coding regio
A:Reference number: A40090; MUID:90161996
A:Accession: C40090
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-528 <CHA>
A:Cross-references: GB:M30441; NID:g199712; PIDN:AAA39716.1; PID:g199713

Query Match 91.0%; Score 71; DB 2; Length 528;
Best Local Similarity 86.7%; Pred. No. 0.0001;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 FAEADDPPTSGFSSIP 15
|||||

Db 371 FAEADDPSSGFNSIP 385

RESULT 6
S09045
potassium channel protein MK-4 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09045
R:Betscholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis
A:Reference number: S09042; MUID:90235950
A:Accession: S09045
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match 80.8%; Score 63; DB 2; Length 57;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Y 1 FAEADDPPTSGFSSIP 15
|||||

Db 11 FAEADDPPTHFQSSIP 25

RESULT 7

A39922 potassium channel KCNA4 - human

N:Alternate names: potassium channel HK1; potassium channel PCN2; shaker-related potassium channel RK3

C:Species: Homo sapiens (man)

C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 05-Nov-1999

C:Accession: A39922; S12630; I77465

R:Tamkun, M.M.; Knoch, K.M.; Walbridge, J.A.; Kroemer, H.; Roden, D.M.; Glover, D.M.

FASEB J. 5, 331-337, 1991

A:Title: Molecular cloning and characterization of two voltage-gated K(+) channel cDNAs

A:Reference number: A39922; MUID:91160866

A:Accession: A39922

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-653 <TAM>

A:Cross-references: GB:M60450; NID:9308762; PIDN:AAA61275.1; PID:9308763

R:Phillipson, L.H.; Schaefer, K.; Lamendola, J.; Bell, G.I.; Steiner, D.F.

Nucleic Acids Res. 18, 7160, 1990

A:Title: Sequence of a human fetal skeletal muscle potassium channel cDNA related to RCK

A:Reference number: S12630; MUID:91088321

A:Accession: S12630

A:Molecule type: mRNA

A:Residues: 1-37, 'R', '39-41', 'R', '43-83', 'EEEAR', '89-303', 'D', '305-541', 'V', '543-630', 'A', '632-653

A:Cross-references: EMBL:M55514; NID:9189659; PIDN:AAA60034.1; PID:9189660

R:Ramashram, M.; Gautam, M.; Kamb, A.A.; Rudy, B.; Tanouye, M.A.; Mathew, M.K.

Mol. Cell. Neurosci. 1, 214-223, 1990

A:Title: Human potassium channel genes: molecular cloning and functional expression.

A:Reference number: I77465

A:Accession: I77465

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-653 <RES>

A:Cross-references: GB:L02751; NID:9186666; PIDN:AAA6140.1; PID:9186667

C:Genetics:

A:Gene: GDB:KCNA4

A:Cross-references: GDB:126730; OMIM:176266

A:Map position: 11p14-11p14

C:Keywords: glycoprotein; phosphoprotein; potassium channel; transmembrane protein; volt

Query Match 75.6%; Score 59; DB 2; Length 653;

Best Local Similarity 73.3%; Pred. No. 0.018;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADDPSTGSSIP 15

|||||:|:| |

DB 498 FAADDEPTTFOSIP 512

RESULT 8

S11049 potassium channel protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

C:Accession: S11049

R:Tsen, C.-C.; Tsen, G.-N.; Schwartz, A.; Tanouye, M.A.

FEBS Lett. 268, 63-68, 1990

A:Title: Molecular cloning and functional expression of a potassium channel cDNA isolate

A:Reference number: S11049; MUID:90446174

A:Accession: S11049

A:Molecule type: mRNA

A:Residues: 1-654 <TSE>

A:Cross-references: GB:M32867; NID:9205042; PIDN:AAA41469.1; PID:9205043

Query Match 75.6%; Score 59; DB 2; Length 654;

Best Local Similarity 73.3%; Pred. No. 0.018;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADDPSTGSSIP 15

|||||:|:| |

DB 499 FAADDEPTTFOSIP 513

RESULT 9

E39113 potassium channel KVL4 - rat

N:Alternate names: potassium channel RK3; shaker-related potassium channel RCK4

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 05-Nov-1999

C:Accession: E39113; S06710

R:Roberts, S.L.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 88, 1798-1802, 1991

A:Title: Cloning and tissue-specific expression of five voltage-gated potassium chan

A:Reference number: A39113; MUID:91156694

A:Accession: E39113

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-654 <ROB>

R:Stuehmer, W.; Ruppersberg, J.P.; Schroeter, K.H.; Sakmann, B.; Stocker, M.; Giese,

EMBO J. 8, 3235-3244, 1989

A:Title: Molecular basis of functional diversity of voltage-gated potassium channels

A:Reference number: S06708; MUID:90059914

A:Accession: S06710

A:Molecule type: mRNA

A:Residues: 1-41, 'A', '43-83', 'EEEAR', '89-94', 'K', '95-654 <STU>

A:Cross-references: EMBL:X16002; NID:957036; PIDN:CAA34133.1; PID:957037

C:Keywords: glycoprotein; phosphoprotein; potassium channel; tetramer; transmembrane

F:309-327/Domain: transmembrane #status predicted <TM1>

F:372-393/Domain: transmembrane #status predicted <TM2>

F:405-424/Domain: transmembrane #status predicted <TM3>

F:425-462/Domain: transmembrane #status predicted <TM4>

F:479-498/Domain: transmembrane #status predicted <TM5>

F:514-523/Domain: transmembrane beta strand #status predicted <TM6>

F:524-532/Domain: transmembrane beta strand #status predicted <TM7>

F:540-562/Domain: transmembrane #status predicted <TM8>

F:533/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:600/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status pre

Query Match 75.6%; Score 59; DB 2; Length 654;

Best Local Similarity 73.3%; Pred. No. 0.018;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADDPSTGSSIP 15

|||||:|:| |

DB 499 FAADDEPTTFOSIP 513

RESULT 10

S24125 potassium channel protein - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: S24125

R:Garcia-Guzman, M.; Calvo, S.; Cena, V.; Criado, M.

FEBS Lett. 308, 283-289, 1992

A:Title: Molecular cloning and permanent expression in a neuroblastoma cell line of a

A:Reference number: S24125; MUID:92371645

A:Accession: S24125

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-660 <GAR>

A:Cross-references: EMBL:X57033; NID:9646; PIDN:CAA0349.1; PID:9647

Query Match 75.6%; Score 59; DB 2; Length 660;

Best Local Similarity 73.3%; Pred. No. 0.018;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 FAADDPSTGSSIP 15

|||||:|:| |

DB 506 FAADDEPTTFOSIP 520

```
RESULT 11
S09049
potassium channel protein Hak-7 - hamster (fragment)
C:Accession: JH0166; D39113; 155392
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09049
R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, P.O.
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K+ channels in insulin-producing cells. Analysis by
A:Reference number: S09042; MUID:90235950
A:Accession: S09049
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-49 <BET>

Query Match          64.1%; Score 50; DB 2; Length 49;
Best Local Similarity 73.3%; Pred. No. 0.034;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
|||||: | |||||
Db 3 FAEADNCGSHFSSIP 17

RESULT 12
S12787
potassium channel KCNA2 - human
N:Alternate names: potassium channel HBK2
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12787; S15057
R:Gupe, A.; Schroeder, K.H.; Ruppersberg, J.P.; Stocker, M.; Drewes, T.; Beckh, S.; Por
EMBO J. 9, 1749-1756, 1990
A:Title: Cloning and expression of a human voltage-gated potassium channel. A novel mem
A:Reference number: S12786; MUID:90269208
A:Accession: S12787
A:Molecule type: mRNA
A:Residues: 1-529 <GRU>
A:Cross-references: EMBL:X17622
R:Pongs, O.
submitted to the EMBL Data Library, November 1989
A:Reference number: S15057
A:Accession: S15057
A:Molecule type: mRNA
A:Residues: 1-57, 'T', '59-529 <PON>
A:Cross-references: EMBL:X17622; NID:932032; PIDN:CAA35623.1; PID:932033
C:Genetics:
A:Gene: GDB:KCNA2; HK4; KVL2
A:Cross-references: GDB:128062; OMIM:176262
C:Keywords: glycoprotein; ion channel; transmembrane protein
F:175-193/Domain: transmembrane #status predicted <TM1>
F:263-384/Domain: transmembrane #status predicted <TM2>
F:296-316/Domain: transmembrane #status predicted <TM3>
F:340-359/Domain: transmembrane #status predicted <TM4>
F:376-395/Domain: transmembrane #status predicted <TM5>
F:457-458/Domain: transmembrane #status predicted <TM6>

Query Match          62.8%; Score 49; DB 2; Length 529;
Best Local Similarity 73.3%; Pred. No. 0.84;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
|||||: | |||||
Db 396 FAEADDDSLFSSIP 410

RESULT 13
JH0166
potassium voltage-gated channel - rat
N:Alternate names: potassium channel RK4; shaker-related potassi
C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 05-Nov-1999
C:Accession: JH0166; D39113; 155392
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09042
R:Betsholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren,
FEBS Lett. 263, 121-126, 1990
A:Title: Expression of voltage-gated K+ channels in insulin-producing cells. Analysis by
A:Reference number: S09042; MUID:90235950
A:Accession: S09042
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-57 <BET>

Query Match          61.5%; Score 48; DB 2; Length 57;
Best Local Similarity 66.7%; Pred. No. 0.092;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 FAEADPTGFSFSSIP 15
|||||: | |||||
```


Db 11 FAEEAEESHFSIP 25

RESULT 15

S09043

potassium channel protein MK-2 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993

C:Accession: S09043

R:Beuscholtz, C.; Baumann, A.; Kenna, S.; Ashcroft, F.M.; Ashcroft, S.J.H.; Berggren, P.O.
FEBS Lett. 263, 121-126, 1990

A:Title: Expression of voltage-gated K⁺ channels in insulin-producing cells. Analysis by

A:Reference number: S09042; MUID:90235950

A:Accession: S09043

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-57 <BET>

Query Match

61.5%; Score 48; DB 2; Length 57;

Best Local Similarity 73.3%; Pred.No. 0.092;

Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAEDDPTSGFSIP 15

||||| | | | |

Db 11 FAEDDPTSLFSP 25

Search completed: February 2, 2001, 10:37:14
Job time: 87 sec

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:38:03 ; Search time 45.64 Seconds
(without alignments)
11.238 Million cell updates/sec

Title: US-09-273-217-4
Perfect score: 78
Sequence: 1 FAHADPTSGFSSIP 15

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries.

Database :

A.Geneseq.36:*

- 1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	15	20	Y42765 Rat potassium chan
2	48.5	62.2	476	20	Y28674 Arabidopsis GRP cy
3	48	61.5	495	20	Y32014 Human cation chan
4	46	59.0	15	20	Y42762 Rat potassium chan
5	43	55.1	597	12	R12384 Bovine pancreatic
6	41	52.6	49	13	R28600 Sequence of a modi
7	41	52.6	78	15	R62361 Synthetic "King Ko
8	41	52.6	78	16	R80094 Synthetic "King Ko
9	41	52.6	575	13	R30045 gE gene deletion f
10	41	52.6	575	15	R47175 Sequence of polype
11	41	52.6	575	16	R82214 Bovine herpesvirus
12	41	52.6	617	14	R31956 Sequence encoded b

13	41	52.6	617	16	R79036
14	40	51.3	535	15	R58985
15	40	51.3	538	16	R75098
16	40	51.3	538	17	W10058
17	40	51.3	546	15	R58981
18	40	51.3	568	15	R58982
19	40	51.3	568	17	R99258
20	40	51.3	668	15	R58983
21	40	51.3	668	15	R70145
22	40	51.3	722	15	R58984
23	40	51.3	722	16	R75107
24	40	51.3	722	17	W10050
25	40	51.3	722	17	R98926
26	40	51.3	742	12	R14311
27	40	51.3	742	17	R98927
28	40	51.3	744	15	R45189
29	40	51.3	745	13	R20098
30	40	51.3	745	15	R58980
31	40	51.3	745	17	R99257
32	40	51.3	745	20	R32168
33	40	51.3	858	20	Y32015
34	39	50.0	51	14	R38802
35	39	50.0	77	14	R38797
36	39	50.0	454	20	Y34779
37	39	50.0	490	20	Y34121
38	39	50.0	491	21	Y70454
39	39	50.0	491	21	Y53780
40	39	50.0	616	20	Y32013
41	38	48.7	109	21	Y64595
42	38	48.7	267	19	W81726
43	38	48.7	267	19	W64359
44	38	48.7	267	20	Y39156
45	38	48.7	267	20	Y39013

ALIGNMENTS

RESULT 1
Y42765 standard; peptide: 15 AA.
Y42765:
20-DEC-1999 (first entry)
Rat potassium channel Kv1.3 vestibule-derived peptide #4.
Ion channel; potassium channel; vestibule; inhibitor; antibody;
polycationic; antagonist; hypertension; cardiac ischemia;
bronchial constriction; neurological diseases.
Synthetic.
Rattus sp.
W09948927-A1.
30-SEP-1999.
19-MAR-1999; 99WO-US06019.
25-MAR-1998; 98US-0079268.
(CORR) CORNELL RES FOUND INC.
Huang X;
WPI; 1999-601205/51.
Designing specific blockers that bind to the external vestibule region
of ion channels, potentially useful for treating e.g. hypertension
Claim 9; Page 9; 40pp; English.

Infectious bovine
Bile salt-stimulat
Recombinant bile s
Human wild-type bi
Bile salt-stimulat
Bile salt-stimulat
Human bile salt-st
Bile salt-stimulat
Bile salt-stimulat
Bile salt-activate
Human bile salt-ac
Human bile salt-ac
Human milk bile-sa
Human bile salt-ac
BSSL/CEU. Homo sa
Bile-salt stimulat
Bile salt-stimulat
Human bile salt-st
Human bile salt-st
Human cation chann
King Kong conotoxi
Conotoxin preprope
Chlamydia pneumoni
Human potassium ch
Human membrane cha
A human voltage-ga
Drosophila melanog
Nonclassical cadhe
M. tuberculosis im
Mycobacterium tube
M. tuberculosis an
M. tuberculosis re

XX This sequence represents a peptide (#4), derived from the
 CC extracellular vestibule portion of the rat potassium channel Kv1.3.
 CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to
 CC generate polyclonal antibodies. The vestibule portion of potassium
 CC channels is located on the extracellular portion of the channel protein,
 CC and generally comprises a loop between the S5 transmembrane domain and
 CC the pore forming region of the channel, or between the pore forming
 CC region and the S6 transmembrane domain. The antibodies generated against
 CC vestibule peptides act as potassium channel inhibitors by binding to the
 CC vestibule portion, physically blocking the pore, or otherwise inducing a
 CC conformational change in the channel. These potassium channel blockers
 CC are potential therapeutic agents for e.g., hypertension, cardiac
 CC ischaemia, bronchial constriction and neurological diseases. Such
 CC inhibitors are specific for particular types of ion channel, and
 CC are produced by rational design based on known nucleotide and amino acid
 CC sequences for ion channels.

XX Sequence 15 AA:

Query Match 100.0%; Score 78; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
 ID Y28674 standard; Protein; 476 AA.
 XX Y28674;
 AC Y28674;
 DT 26-OCT-1999 (first entry)
 DE Arabidopsis GTP cyclohydrolase II/DHP synthase.
 XX

XX Bifunctional enzyme: GTP cyclohydrolase II; DHP synthase; herbicide;
 KM 3,4-dihydroxy-2-butanone-4-phosphate synthase; riboflavin biosynthesis;
 KM 2,5-diamino-4-oxy-6-ribosylamino-pyrimidine-5-phosphate; GTP; Shuffled;
 KM ribulose-5-phosphate; 3,4-dihydroxy-2-butanone phosphate; inhibitor;
 KM Arabidopsis thaliana Expressed Sequence Tag database; Bacillus subtilis;
 KM enhanced tolerance.

XX Arabidopsis thaliana.

XX MO938986-A2.

XX 05-AUG-1999.

XX 28-JAN-1999; 99MO-EP00556.

XX 30-JAN-1998; 98US-0109810.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.

XX Bruun SA, Guyer CD, Johnson MA, Volrath SL, Ward ER;

XX WPI; 1999-479193/40.

XX N-PSDB; X80820.

XX New isolated riboflavin biosynthesis genes, used to identify

XX compounds for use, e.g. as herbicides

XX Claim 49; Page 71-73; 78pp; English.

XX The present sequence is bifunctional enzyme GTP cyclohydrolase II/
 CC 3,4-dihydroxy-2-butanone-4-phosphate synthase (DHP synthase). GTP cyclo
 CC hydrolase II is the first enzyme of riboflavin biosynthesis, catalysing

CC the synthesis of 2,5-diamino-4-oxy-6-ribosylamino-pyrimidine-5-phosphate
 CC from GTP. DHP synthase catalyses the conversion of ribulose 5 phosphate
 CC to 3,4-dihydroxy-2-butanone phosphate (DHP). A cDNA sequence was derived
 CC from Arabidopsis thaliana Expressed Sequence Tag database and showed
 CC homology to the bifunctional GTP cyclohydrolase II/DHP synthase of
 CC Bacillus subtilis. The purified enzyme can be used to screen for novel
 CC inhibitors which can be used as herbicides to suppress the
 CC growth of undesirable vegetation. The encoding nucleotide sequence can
 CC be shuffled to produce an enzyme that confers on plants, enhanced
 CC tolerance to herbicides in an amount that normally inhibits riboflavin
 CC biosynthesis. This can be used to selectively suppress the growth of
 CC weeds.

XX Sequence 476 AA;

Query Match 62.2%; Score 48.5; DB 20; Length 476;
 Best Local Similarity 63.2%; Pred. No. 0.64;
 Matches 12; Conservative 0; Mismatches 2; Indels 5; Gaps 1;

QY 2 AEADD-----PTSGFSSIP 15
 ID Y32014 standard; Protein; 495 AA.
 XX Y32014;
 AC Y32014;
 DT 05-JAN-2000 (first entry)
 DE Human cation channel protein.
 XX

XX Cation channel protein; CCP; ion transport; arrhythmia;
 KM diabetes mellitus; seizure; asthma; hypertension; therapy;
 KM protein engineering; human.
 XX

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 61..119 /note="crystal region"

XX MO9947923-A2.

XX 23-SEP-1999.

XX 22-MAR-1999; 99MO-US06307.

XX 20-MAR-1998; 98US-0045529.

XX 02-APR-1998; 98US-0054347.

XX (UIRQ) UNIV ROCKEFELLER.

XX Mackinnon R;

XX WPI; 1999-601131/51.

XX Assays for screening compounds which interact with cation channel

XX proteins, useful for providing agents for treatment of diseases

XX Claim 21; Page 135-137; 165pp; English.

XX The present sequence represents a human cation channel protein
 CC (CCP). The invention provides an assay for screening potential
 CC drugs or agents which interact with CCPs using prokaryotic CCPs
 CC (such as those given in Y32009-12) mutated, using recombinant DNA
 CC technology, to mimic the physiological function and chemical
 CC properties of a functional eukaryotic CCP (such as those given in
 CC Y32013-22). An example of a mutated prokaryotic CCP is given in
 CC Y32024. The crystal region of the CCP may also be used in the

CC assay. The drugs or agents obtained can be used to treat
 CC conditions related to the function of CCP in vivo, such as cardiac
 CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
 CC hypertension. The invention has overcome the physical limitations
 CC regarding the isolation and purification of eukaryotic CCPs.

SQ Sequence 495 AA;

Query Match 61.5%; Score 48; DB 20; Length 495;
 Best Local Similarity 66.7%; Pred. No. 0.83;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 346 faaeaaeshssip 360

RESULT 4
 Y42762

ID Y42762 standard; peptide: 15 AA.

XX Y42762;

DT 20-DEC-1999 (first entry)

XX Rat potassium channel Kv1.2 vestibule-derived peptide #1.

DE Ion channel; potassium channel; vestibule; inhibitor; antibody;

XX polyclonal; antagonist; hypertension; cardiac ischemia;

KW bronchial constriction; neurological diseases.

XX Synthetic.

OS Rattus sp.

PN W09948927-A1.

XX 30-SEP-1999.

PD 19-MAR-1999; 99WO-US06019.

XX 25-MAR-1998; 98US-0079268.

XX (CORR) CORNELL RES FOUND INC.

XX Huang X;

PI WPI: 1999-601205/51.

XX Designing specific blockers that bind to the external vestibule region

PT of ion channels, potentially useful for treating e.g. hypertension

XX Claim 9; Page 8; 40pp; English.

PS This sequence represents a peptide (#1), derived from the extracellular

CC vestibule portion of the rat delayed rectifier potassium channel Kv1.2.

CC This was conjugated to keyhole limpet haemocyanin (KLH) and used to

CC generate polyclonal antibodies. The vestibule portion of potassium

CC channels is located on the extracellular portion of the channel protein,

CC and generally comprises a loop between the S5 transmembrane domain and

CC the pore forming region of the channel, or between the pore forming

CC region and the S6 transmembrane domain. The antibodies generated against

CC vestibule peptides act as potassium channel inhibitors by binding to the

CC conformational change in the channel. These potassium channel blockers

CC are potential therapeutic agents for e.g., hypertension, cardiac

CC ischaemia, bronchial constriction and neurological diseases. Such

CC inhibitors are specific for particular types of ion channel, and

CC are produced by rational design based on known nucleotide and amino acid

CC sequences for ion channels.

XX Sequence 15 AA;

Query Match 59.0%; Score 46; DB 20; Length 15;
 Best Local Similarity 66.7%; Pred. No. 0.034;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 1 faeaderdsqfssip 15

RESULT 5
 ID R12384
 R12384 standard; Protein: 597 AA.

XX R12384;

DT 14-AUG-1991 (first entry)

DE Bovine pancreatic cholesterol esterase.

XX Cholesterol; PCE; atherosclerosis.

XX Bos taurus.

XX W09107483-A.

XX 30-MAY-1991.

XX 13-NOV-1990; 90WO-US06483.

XX 13-NOV-1989; 89US-0434899.

XX (LANG/) LANGE L G.

XX Lange LG, Spillburg CA;

XX WPI: 1991-178095/24.

XX N-PSDB: Q11977.

XX Method for purifying pancreatic cholesterol esterase - gene

XX encoding it for expression in cells used e.g. to screen

XX inhibitors, decrease cholesterol absorption, etc.

XX Disclosure: fig 1; 28pp; English.

XX This recombinant bovine pancreatic cholesterol esterase (PCE) is

CC purified to homogeneity (claimed) using a sulphated matrix. It

CC can be used to produce esterified cholesterol from free fatty

CC acids and free cholesterol or to break down cholesteryl-fatty

CC acids by altering the taurocholate concn. Thus it can be used

CC to alter the cholesterol/cholesterol ester compsn. of food

CC stuffs and biologics. It can also be used to produce antibodies

CC (e.g. by immunising cows and purifying the antibodies from their

CC milk) which can be used as inhibitors to PCE which may lead to

CC reduced serum cholesterol levels.

CC See also Q11978-79 and R12385-86.

XX Sequence 597 AA;

QY Query Match 55.1%; Score 43; DB 12; Length 597;
 Best Local Similarity 46.7%; Pred. No. 8.5;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Db 1 FAEADPTSGFSSIP 15
 |||||:|||||
 Db 489 fatgqntcncstcp 503

RESULT 6
 R28600
 ID R28600 standard; Protein: 49 AA.

```

AC R28600;
XX
XX 21-MAR-1993 (first entry)
XX
XX Sequence of a modified filamentous phage coat protein membrane anchor
DE cpvIII.
XX
XX Filamentous phage; coat protein membrane anchor; cpvIII.
XX
XX Filamentous phage.
XX
XX WO9218619-A.
XX
XX 29-OCT-1992.
XX
XX 10-APR-1992; 92WO-US03091.
XX
XX 10-APR-1991; 91US-0683602.
XX
XX 27-JAN-1992; 92US-0826623.
XX
XX (SCRI ) SCRIpps RES INST.
XX
XX Barbas C, Kang A, Lerner RA.
XX
XX WPI; 1992-382106/46.
XX
XX Filamentous phage expressing hetero:dimeric receptor - esp.
XX antibody, in its coat protein, useful for diagnostic assay, also
XX new phage DNA libraries and mutagenic oligo:nucleotide primers
XX
XX Example; Page 187; 229pp; English.
XX
XX M13mp18 was used as a source for isolating the gene encoding
XX cpvIII. The sequence of the gene encoding the membrane anchor
XX domain of cpvIII (see Q30709) was modified through PCR
XX amplification to incorporate the restriction endonuclease sites
XX Spe I and EcoR I and two stop codons prior to the EcoR I site.
XX The corresp. amino acid residue sequence of the membrane anchor
XX domain of cpvIII is given in R28600.
XX
XX Sequence 49 AA:

Query Match 52.6%; Score 41; DB 13; Length 49;
Best Local Similarity 53.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEADDPSTGFSST 14
   ||||| 1:1
Db 1 aegddpakafns1 13

RESULT 7
R62361
ID R62361 standard; Protein; 78 AA.
XX
XX R62361;
XX
XX 04-MAY-1995 (first entry)
XX
XX Synthetic "King Kong" (KK-O) conotoxin.
XX
XX Conotoxin; toxin; insecticide; Baculovirus; gastropod; neurotoxin;
XX Conus textile; KK-O.
XX
XX Synthetic.
XX
XX GB2276622-A.
XX
XX 05-OCT-1994.
XX
XX 25-MAR-1994; 94GB-0006032.
XX

```

```

PR 26-MAR-1993; 93GB-0006295.
XX
XX (GUES/) GUEST P J.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Earley FGP, Guest PJ, Suter M, Windass JD;
XX
XX WPI; 1994-296384/37.
XX
XX N-PSDB; Q73314, Q73320.
XX
XX New synthetic DNA encoding mollusc-derived insecticidal toxin -
XX and related transfer vectors, host cells and plants; useful as
XX biological insect control agents
XX
XX Claim 1; Figure 1; 75pp; English.
XX
XX The conotoxins are low molecular weight neuroactive peptides
XX isolated from the Conus genus of marine gastropods. They have a
XX very diverse range of biological effects. Some of these conotoxins
XX exhibit insecticidal activity. This synthetic sequence of the Conus
XX textile derived protein KK-O was expressed in Baculovirus (AcMNPV)
XX expression systems and was found to be capable of significantly
XX shortening the time a baculovirus takes to incapacitate susceptible
XX insect hosts.
XX
XX Sequence 78 AA:

Query Match 52.6%; Score 41; DB 15; Length 78;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 FAADDPSTGFSST 14
   ||||| 1:1
Db 19 fatadpgrnglgnl 32

RESULT 8
R80094
ID R80094 standard; Protein; 78 AA.
XX
XX R80094;
XX
XX 09-MAY-1996 (first entry)
XX
XX Synthetic "King Kong" (SKK-O) conotoxin.
XX
XX Insecticide; recombinant baculovirus; polyhedrin; heterologous;
XX gene; AcMNPV virus; King Kong; conotoxin gene; SKK-O.
XX
XX Synthetic.
XX
XX WO9526410-A2.
XX
XX 05-OCT-1995.
XX
XX 27-MAR-1995; 95WO-GB00677.
XX
XX 25-MAR-1994; 94GB-0005951.
XX
XX (ZENE ) ZENECA LTD.
XX
XX Windass JD;
XX
XX WPI; 1995-351327/45.
XX
XX N-PSDB; T04668.
XX
XX New insecticidal recombinant baculovirus - comprises a polyhedron
XX gene and a heterologous gene expressing an insecticidal protein with
XX different promoters
XX
XX Example 2; Page 31; 58pp; English.
XX

```

CC A novel insecticidal recombinant baculovirus comprises a polyhedrin
 CC gene and a heterologous gene, encoding an insecticidal protein,
 CC under the control of different promoters. A specific example is a
 CC recombinant AcMNPV virus carrying the synthetic "King Kong"
 CC conotoxin gene (SKK-O) T04668 (which encodes R80094) under the
 CC transcriptional control of the polyhedrin promoter, and an active
 CC polyhedrin gene under the control of the p10 promoter.

XX Sequence 78 AA:

Query Match 52.6%; Score 41; DB 16; Length 78;
 Best Local Similarity 50.0%; Pred. No. 1.9;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 AEADDPGSGFSSIP 14
 ||||| : :
 Db 19 fatadddprnglgnl 32

RESULT 9

R30045 R30045 standard; Protein; 575 AA.

XX R30045;

DT 29-APR-1993 (first entry)

DE gE gene deletion from mutant bovine herpes virus type 1.

KW BHV-1; cattle; cows; bos taurus; glycoprotein gene; vaccines;
 immunise; vaccinate; diagnosis; testing.

XX Bovine herpes virus type 1.

OS Key Location/Qualifiers

FT Region 1..26 /note="Eukaryotic export signal"

FT Region 423..450 /note="transmembrane region"

PN WO9221751-A.

PD 10-DEC-1992.

PF 05-JUN-1992; 92WO-NL00097.

PR 07-JUN-1991; 91NL-0000989.

PA (DIER-) STICHTING CENT DIERGENESKUNDIG INST.

XX Maes RK, Rijsewijk FAM, Van Oirschot JT;

XX WPI: 1992-433650/52.

DR N-NSDB; Q32857.

PT Mutant bovine herpes virus with deleted glyco-protein gene - used
 PT for vaccination against and diagnosis of bovine herpes virus type
 PT 1

PS Claim 1; Page 46; 84pp; English.

XX This sequence represents the area around a deletion of the gE gene
 CC in the Difivac-1 strain of bovine herpes virus type 1. It was
 CC decoded from the appropriate DNA, isolated as detailed in Q32857.
 CC Sequence analysis showed that this amino acid sequence has the
 CC characteristics of a transmembrane glycoprotein. The first 26 amino
 CC acids are recognised as a typically eukaryotic export signal and the
 CC area between 423 and 450 is recognised as a transmembrane region.
 CC In addition, three potential N-bound glycosylation sites occur in
 CC this sequence. This predicted amino acid sequence exhibits clear
 CC similarities to the glycoprotein gE-gene of herpes simplex virus
 CC (HSV). For this and other similarities found the gene is called the

CC BHV-1 gE gene.
 XX Sequence 575 AA:

Query Match 52.6%; Score 41; DB 13; Length 575;
 Best Local Similarity 57.1%; Pred. No. 19;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEADDPGSGFSSIP 15
 ||||| : :
 Db 516 agapeptsgfarap 529

RESULT 10

R47175 R47175 standard; Protein; 575 AA.

XX R47175;

DT 20-JUL-1994 (first entry)

DE Sequence of polypeptide encoded by the second open reading frame in
 DE the unique short (US) region of bovine herpes virus (BHV) genome.

XX Insertion region; unique short region; US; vaccine; antigen.

OS Bovine herpes virus type 1, strain ST.

PN WO9400586-A.

PD 06-JAN-1994.

PF 25-JUN-1993; 93WO-FR00642.

PR 26-JUN-1992; 92FR-0007930.

PA (INMR) RHONE MERIEUX SA.

XX Audonnet JF, Legastelois ICMA, Leung-tack P, Riviere MEA;

DR WPI: 1994-026222/03.

XX N-PSDB; Q53350.

PT New insertion region sequence of bovine herpes virus genomic DNA
 PT - used for recombinant virus with this region deleted or
 PT inactivated, useful in vaccines allowing differentiation between
 PT vaccinated and infected cattle

PS Claim 9; Fig 2; 47pp; French.

XX The 4190 bp sequence in Q53350 encodes polypeptides homologous to
 CC HSV-1 gI, gE and US9; these are neither essential for in vitro
 CC replication nor important in inducing a protective immune response.
 CC It is genomic DNA purified from the ST strain of BHV-1. (BHV is also
 CC known as infectious bovine rhinotracheitis virus.). The sequence
 CC forms the insertion region in genomic DNA. RBHV in which the
 CC specific insertion region, esp. nucleotides 172-1311, has been
 CC deleted or inactivated by insertion are claimed.

XX Sequence 575 AA:

Query Match 52.6%; Score 41; DB 15; Length 575;
 Best Local Similarity 57.1%; Pred. No. 19;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEADDPGSGFSSIP 15
 ||||| : :
 Db 516 agapeptsgfarap 529

RESULT 11

```
R82214
ID   R82214 standard; Protein; 575 AA.
AC   R82214;
XX
XX
DT   10-APR-1996 (first entry)
XX
DE   Bovine herpesvirus-1 FM gII glycoprotein.
XX
XX   Glycoprotein, mutant; bovine herpesvirus; vaccine; antigen;
KM   antigenic; bovine rhinotracheitis virus; IBRV; BHV; gII;
KM   immunisation; vaccination.
XX
XX   Bovine herpesvirus.
OS
XX   EP68356-A2.
PN
XX
PD   23-AUG-1995.
XX
XX   31-JAN-1995; 95EP-0870007.
PF
XX
PR   31-JAN-1994; 94ES-0000172.
XX
XX   (HPR-) LAB HPRFA SA.
PA
XX   Lloberas J, Perez-pons JA, Pinol J, Querol E, Rebordosa X;
PI
XX   WPI: 1995-284793/38.
DR   N-PSDB; T03824.
XX
XX   New infectious bovine rhinotracheitis virus mutants - contain a
PT   mutation in the glyco-protein gII gene, used to produce vaccines to
PT   prevent infection
XX
XX   Disclosure; Page 20-24; 33pp; English.
PS
XX
XX   The bovine herpesvirus-1 (BHV-1) FM gII glycoprotein gene can be
CC   mutated by an insertion, deletion or substitution to produce a
CC   BHV-1 FM gII- phenotype of an infectious bovine rhinotracheitis
CC   virus (IBRV) which then fails to produce any antigenic gII
CC   glycoprotein. These mutated viruses can then be used in vaccines
CC   which are capable of eliciting both humoral and cellular responses
CC   in the immunised animal. Vaccinated animals can be distinguished
CC   serologically from animals infected with field strains of IBRV.
XX
XX   Sequence 575 AA;
SQ
```

```
PD   04-FEB-1993.
XX
XX   20-JUL-1992; 92WO-US06034.
PF
XX
XX   18-JUL-1991; 91US-0732584.
PR
XX
XX   (SYTR ) SYNTRO CORP.
PA
XX
XX   Cochran MD, Macdonald RD;
PI
XX
XX   WPI: 1993-058725/07.
DR   N-PSDB; Q36769.
XX
XX
XX   Recombinant infectious bovine rhinotracheitis virus - provides
PT   isolated DNA encoding gPE glyco:protein, gPG glyco:protein and
PT   unique short 2 genes of the virus
XX
XX   Example; Fig 15; 240pp; English.
PS
XX
XX   The sequence of 2038 base pairs of the IBR unique short
CC   region, starting approximately 1325 base pairs upstream in the
CC   HindIII K/HindIII F junction in the HindIII K fragment, are shown.
CC   The glycoprotein E (gPE) gene is transcribed toward the HindIII
CC   K/HindIII F junction.
XX
XX   Sequence 617 AA;
SQ
```

```
Query Match 52.6%; Score 41; DB 14; Length 617;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 AEADDPGSGSSIP 15
   | | :|||||: |
Db 558 agapeptsgfarap 571

RESULT 13
ID R79036 standard; Protein; 617 AA.
XX
XX   R79036;
AC
XX
XX   15-APR-1996 (first entry)
DT
XX
DE   Infectious bovine rhinotracheitis virus glycoprotein E gene product.
XX
XX   Bovine herpesvirus-1; infectious bovine rhinotracheitis virus;
KM   IBR; bovine respiratory disease; shipping fever; vaccine; vector;
KM   attenuation; glycoprotein E.
XX
XX   Bovine herpesvirus-1 strain Cooper isolate S-IBR-000.
OS
XX
XX   Key Location/Qualifiers
FH
XX   Key MISC-difference 52
FT
XX   MISC-difference 52 /note= "amino acid at position 52 is not
FT
XX   MISC-difference 458 identified in the specification"
FT
XX   MISC-difference 458 /note= "amino acid at position 458 is not
FT
XX   MISC-difference 458 identified in the specification"
XX
XX   WO9521261-A1.
XX
XX   10-AUG-1995.
PD
XX
XX   02-FEB-1995; 95WO-US01491.
PF
XX
XX   04-FEB-1994; 94US-0191866.
PR
XX
XX   (SYTR ) SYNTRO CORP.
PA
XX
XX   Cochran MD;
PI
XX
```


DR WPI; 1995-283781/37.
 DR N-PSDB; Q97671.
 XX
 PT Novel recombinant infectious bovine rhinotracheitis virus - used in
 PT vaccines to immunise animals against bovine respiratory disease
 PT complex
 XX
 PS Disclosure: Page 191-193; 301pp; English.
 XX
 CC The glycoprotein G (gE) (R79036) of infectious bovine rhinotracheitis
 CC (IBR) virus strain Cooper (isolate S-IBR-000) is encoded by DNA
 CC (Q97671) in plasmid pSV1645. Deletion of the gE gene attenuates IBR
 CC virus and provides a novel serological marker for differentiating the
 CC virus from wild-type virus. Novel foetal-safe, live, recombinant IBR
 CC viruses, e.g. S-IBR-052 (ATCC VR 2443), were constructed that were
 CC attenuated by deletion of the US2, gC and/or gE genes and which included
 CC DNA coding for infectious disease pathogen antigens. The recombinant
 CC vaccines are used to protect cattle against bovine respiratory disease
 CC complex (shipping fever).
 XX
 SQ Sequence 617 AA;
 Query Match 52.6%; Score 41; DB 16; Length 617;
 Best Local Similarity 57.1%; Pred. No. 21;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 OY 2 AEADPTSGFSSIP 15
 Db 558 agapeptsgfarap 571
 RESULT 14
 ID R58985 standard; protein: 535 AA.
 AC R58985;
 XX
 DT 03-MAY-1995 (first entry)
 XX
 DE Bile salt-stimulated lipase (variant A).
 XX
 KW Bile salt stimulated lipase; BSSL; glycoprotein; esterase;
 KW acetyl cholinesterase; cystic fibrosis; chronic pancreatitis;
 KW fat malabsorption; vitamins; dietary lipids; food supplement.
 XX
 OS Homo sapiens.
 XX
 PN WO9420610-A.
 XX
 PD 15-SEP-1994.
 XX
 PF 25-FEB-1994; 94WO-SE00160.
 XX
 PR 01-MAR-1993; 93SE-0000686.
 PR 04-MAR-1993; 93SE-0000722.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Blackberg L, Edlund M, Hansson L, Kernell O, Lundberg L;
 PI Stromqvist M, Toernell J;
 XX
 DR WPI; 1994-303018/37.
 XX
 PT Bile salt-stimulated lipase variants and coding sequences - used
 PT to produce prods. for treatment of a pathological condition
 PT related to exocrine pancreatic insufficiency
 XX
 PS Example 1.1.2; Page 57-58; 102pp; English.
 XX
 CC Bile salt-stimulated lipase (BSSL) is a single chain glycoprotein
 CC which is highly glycosylated. The N-terminal half of the protein
 CC shows a homology to acetyl cholinesterase and some other esterases.

CC BSSL variant polypeptides can be used for the treatment of a
 CC pathological condition related to exocrine pancreatic insufficiency
 CC such as cystic fibrosis, chronic pancreatitis, fat malabsorption or
 CC malabsorption of fat soluble vitamins for improvement of utilisation
 CC of dietary lipids, particularly in preterm born infants. They can
 CC also be used as supplements for infant food formulations. The BSSL
 CC variants have maintained catalytic activity but contain less
 CC glycosylation sites than native BSSL. This variant is a deletion
 CC mutant lacking the C-terminal 187 amino acids of the wild-type
 CC protein (See R58980).
 CC
 XX
 SQ Sequence 535 AA;
 Query Match 51.3%; Score 40; DB 15; Length 535;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 Db 471 fakgqpmgdsavp 485
 RESULT 15
 ID R75098 standard; Protein: 538 AA.
 AC R75098;
 XX
 DT 26-JAN-1996 (first entry)
 XX
 DE Recombinant bile salt-activated lipase.
 XX
 KW Bile salt activated lipase; BAL; C-terminal repeat.
 XX
 OS Mammalia.
 XX
 PN JP07111891-A.
 XX
 PD 02-MAY-1995.
 XX
 PF 30-SEP-1993; 93JP-0245079.
 XX
 PR 30-SEP-1993; 93JP-0245079.
 XX
 PA (MEIP) MEIJI MILK PROD CO LTD.
 XX
 DR WPI; 1995-196318/26.
 DR N-PSDB; Q90569.
 XX
 PT New recombinant bile salt-activated lipase(s), DNA encoding them
 PT and vectors - useful for high level expression of the lipase(s) by
 PT fermenter-culturing.
 XX
 PS Claim 1; Page 9-10; 31pp; Japanese.
 XX
 CC New lipases are ones in which 1-15 repeats of any of the sequences
 CC R75099-R75105 (encoded by Q90570-Q90576) are attached to the C-
 CC terminus of the bile salt-activated lipase (BAL) of sequence R75098
 CC (encoded by Q90569) and/or in which the amino acid sequence SMRS
 CC (encoded by Q90578) is attached to the N-terminus of the BAL. The
 CC recombinant lipases can be produced by fermentation in *Pichia*
 CC pastoris GS 115 transformed host cells.
 XX
 SQ Sequence 538 AA;
 Query Match 51.3%; Score 40; DB 16; Length 538;
 Best Local Similarity 46.7%; Pred. No. 27;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 OY 1 FAEADPTSGFSSIP 15
 II: II I I::I

Fri Feb 2 15:15:38 2001

Db 471 faktgdpnmgdsavp 485

Search completed: February 2, 2001, 10:38:05
Job time: 138 sec

us-09-273-217-4.rag

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:29 ; Search time 34.98 Seconds
(without alignments)
7.187 Million cell updates/sec

Title: US-09-273-217-3

Sequence: 1 GAOPNDPSASEHTH 14

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCRTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	59.5	271	1	US-08-276-919-10 Sequence 10, Appl
2	47	59.5	271	1	US-08-776-088-13 Sequence 13, Appl
3	47	59.5	271	4	PCT-US95-09145A-13 Sequence 13, Appl
4	47	59.5	274	1	US-08-776-088-15 Sequence 15, Appl
5	47	59.5	274	4	PCT-US95-09145A-15 Sequence 15, Appl
6	47	59.5	325	1	US-08-276-919-4 Sequence 4, Appl
7	47	59.5	325	1	US-08-276-919-13 Sequence 13, Appl
8	47	59.5	325	1	US-08-776-088-4 Sequence 4, Appl
9	47	59.5	325	1	US-08-776-088-18 Sequence 18, Appl
10	47	59.5	325	4	PCT-US95-09145A-4 Sequence 4, Appl
11	47	59.5	325	4	PCT-US95-09145A-18 Sequence 18, Appl
12	47	59.5	354	1	US-08-276-919-2 Sequence 2, Appl
13	47	59.5	354	1	US-08-776-088-2 Sequence 2, Appl
14	47	59.5	354	1	US-08-776-088-6 Sequence 6, Appl
15	47	59.5	354	3	US-09-325-320-2 Sequence 2, Appl
16	47	59.5	354	4	PCT-US95-09145A-2 Sequence 2, Appl
17	47	59.5	354	4	PCT-US95-09145A-6 Sequence 6, Appl
18	44	55.7	434	1	US-08-337-602-2 Sequence 2, Appl
19	44	55.7	434	3	US-08-558-135-2 Sequence 2, Appl
20	38	48.1	98	2	US-08-454-557C-30 Sequence 30, Appl
21	38	48.1	98	2	US-08-340-426D-30 Sequence 30, Appl
22	38	48.1	98	2	US-08-450-673C-30 Sequence 30, Appl
23	38	48.1	98	2	PCT-US95-17111A-30 Sequence 30, Appl
24	37	46.8	266	4	US-07-857-224B-43 Sequence 43, Appl
25	37	46.8	267	2	US-07-857-224B-45 Sequence 45, Appl
26	37	46.8	3218	1	US-08-764-100-27 Sequence 27, Appl
27	36	45.6	302	3	US-08-303-861-20 Sequence 20, Appl
28	36	45.6	396	2	US-08-784-512-3 Sequence 3, Appl

29	36	45.6	403	2	US-09-092-770-4	Sequence 4, Appl
30	36	45.6	403	3	US-09-222-851-4	Sequence 4, Appl
31	36	45.6	488	2	US-08-928-692-11	Sequence 11, Appl
32	36	45.6	507	1	US-08-348-891A-3	Sequence 3, Appl
33	36	45.6	507	2	US-08-905-817-3	Sequence 3, Appl
34	36	45.6	543	1	US-08-362-232-2	Sequence 2, Appl
35	36	45.6	543	1	US-08-814-196-2	Sequence 2, Appl
36	36	45.6	631	1	US-08-605-541B-12	Sequence 12, Appl
37	35	44.3	42	1	US-08-605-449-39	Sequence 39, Appl
38	35	44.3	183	1	US-08-361-467B-11	Sequence 11, Appl
39	35	44.3	183	1	US-08-484-332C-11	Sequence 11, Appl
40	35	44.3	286	1	US-08-382-184-3	Sequence 3, Appl
41	35	44.3	286	2	US-08-641-356-3	Sequence 3, Appl
42	35	44.3	325	1	US-08-382-184-2	Sequence 2, Appl
43	35	44.3	325	2	US-08-641-356-2	Sequence 2, Appl
44	35	44.3	389	1	US-07-939-501A-1	Sequence 1, Appl
45	35	44.3	423	1	US-07-939-501A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-276-919-10
; Sequence 10, Application US/08276919
; Patent No. 5589579
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,919
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Neilligan, Mark C.
; REGISTRATION NUMBER: 36,389
; REFERENCE/DOCKET NUMBER: B35792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-939-4500
; TELEFAX: 214-939-4600
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-919-10

Query Match 59.5%; Score 47; DB 1; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PNDPSASEHT 13
|||||
Db 96 PNDPSASEHT 105

RESULT 2

US-08-776-088-13
: Sequence 13, Application US/08776088
: Patent No. 5773579
: GENERAL INFORMATION:
: APPLICANT: Torczynski, Richard M.
: APPLICANT: Bollon, Arthur P.
: TITLE OF INVENTION: Lung Cancer Marker
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SIDLEY & AUSTIN
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: TX
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/776,088
: FILING DATE: 19-JUL-95
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Eugenia S. Hansen
: REGISTRATION NUMBER: 31,966
: REFERENCE/DOCKET NUMBER: 10365/05011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 214-981-3300
: TELEFAX: 214-981-3400
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-776-088-13

Query Match 59.5%; Score 47; DB 1; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPASEHT 13
|||||

Db 96 PNDPASEHT 105

RESULT 3
PCT-US95-09145A-13
: Sequence 13, Application PC/TUS9509145A
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Lung Cancer Marker
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: TX
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/09145A
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:

NAME: John A. Harre
: REGISTRATION NUMBER: 37,345
: REFERENCE/DOCKET NUMBER: B35792CIPCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 214-939-4500
: TELEFAX: 214-939-4600
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-09145A-13

Query Match 59.5%; Score 47; DB 4; Length 271;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPASEHT 13
|||||

Db 96 PNDPASEHT 105

RESULT 4
US-08-776-088-15
: Sequence 15, Application US/08776088
: Patent No. 5773579
: GENERAL INFORMATION:
: APPLICANT: Torczynski, Richard M.
: APPLICANT: Bollon, Arthur P.
: TITLE OF INVENTION: Lung Cancer Marker
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SIDLEY & AUSTIN
: STREET: 1201 Elm Street, Suite 4500
: CITY: Dallas
: STATE: TX
: COUNTRY: US
: ZIP: 75270-2197
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/776,088
: FILING DATE: 19-JUL-95
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Eugenia S. Hansen
: REGISTRATION NUMBER: 31,966
: REFERENCE/DOCKET NUMBER: 10365/05011
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 214-981-3300
: TELEFAX: 214-981-3400
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 274 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-776-088-15

Query Match 59.5%; Score 47; DB 1; Length 274;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPASEHT 13
|||||

Db 96 PNDPASEHT 105

RESULT 5
PCT-US95-09145A-15
Sequence 15, Application PC/TUS9509145A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09145A
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: John A. Harre
REGISTRATION NUMBER: 37,345
REFERENCE/DOCKET NUMBER: B35792CIPPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-09145A-15

Query Match 59.5%; Score 47; DB 4; Length 274;
Best Local Similarity 80.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||
DB 96 PNDPSASEHT 105

RESULT 6
US-08-276-919-4
Sequence 4, Application US/08276919
Patent No. 5589579
GENERAL INFORMATION:
APPLICANT: Torczynski, Richard M.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
FILING DATE:

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-919-4

Query Match 59.5%; Score 47; DB 1; Length 325;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||
DB 96 PNDPSASEHT 105

RESULT 7
US-08-276-919-13
Sequence 13, Application US/08276919
Patent No. 5589579
GENERAL INFORMATION:
APPLICANT: Torczynski, Richard M.
TITLE OF INVENTION: Lung Cancer Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
STREET: 1201 Elm Street, Suite 4500
CITY: Dallas
STATE: TX
COUNTRY: US
ZIP: 75270-2197
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Nelligan, Mark C.
REGISTRATION NUMBER: 36,389
REFERENCE/DOCKET NUMBER: B35792
TELECOMMUNICATION INFORMATION:
TELEPHONE: 214-939-4500
TELEFAX: 214-939-4600
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-276-919-13

Query Match 59.5%; Score 47; DB 1; Length 325;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||

Db 96 PNDPGESEHT 105

RESULT 8

US-08-776-088-4

Sequence 4, Application US/08776088,
Patent No. 5773579

GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Bollon, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: SIDLEY & AUSTIN

STREET: 1201 Elm street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,088

FILING DATE: 19-JUL-95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Eugenia S. Hansen

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 10365/05011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-981-3300

TELEFAX: 214-981-3400

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-776-088-4

Query Match

Best Local Similarity

Matches

8; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

OY 4 PNDPGESEHT 13

Db 96 PNDPGESEHT 105

RESULT 9

US-08-776-088-18

Sequence 18, Application US/08776088

Patent No. 5773579

GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Bollon, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: SIDLEY & AUSTIN

STREET: 1201 Elm street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,088

FILING DATE: 19-JUL-95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Eugenia S. Hansen

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 10365/05011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-981-3300

TELEFAX: 214-981-3400

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-776-088-18

Query Match

Best Local Similarity

Matches

8; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

OY 4 PNDPGESEHT 13

Db 96 PNDPGESEHT 105

RESULT 10

PCT-US95-09145A-4

Sequence 4, Application PC/TUS9509145A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS

STREET: 1201 Elm street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09145A

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: John A. Harre

REGISTRATION NUMBER: 37,345

REFERENCE/DOCKET NUMBER: B35792CIPCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-939-4500

TELEFAX: 214-939-4600

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-09145A-4

Query Match

Best Local Similarity

Matches

8; Conservative

0; Mismatches

2; Indels

0; Gaps

0;

OY 4 PNDPSASEHT 13
|||||
Db 96 PNDPHGSEHT 105

RESULT 11
PCT-US95-09145A-18

; Sequence 18, Application PC/TUS9509145A
; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS

STREET: 1201 Elm Street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09145A

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: John A. Harre

REGISTRATION NUMBER: 37,345

REFERENCE/DOCKET NUMBER: B35792CIPCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-939-4500

TELEFAX: 214-939-4600

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 325 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-09145A-18

Query Match 59.5%; Score 47; DB 4; Length 325;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||
Db 96 PNDPHGSEHT 105

RESULT 12
US-08-276-919-2

; Sequence 2, Application US/08276919

; Patent No. 5589579

; GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Bollon, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS

STREET: 1201 Elm Street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,919

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Nelligan, Mark C.

REGISTRATION NUMBER: 36,389

REFERENCE/DOCKET NUMBER: B35792

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-939-4500

TELEFAX: 214-939-4600

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 354 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-276-919-2

Query Match 59.5%; Score 47; DB 1; Length 354;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PNDPSASEHT 13
|||||
Db 125 PNDPHGSEHT 134

RESULT 13
US-08-776-088-2

; Sequence 2, Application US/08776088

; Patent No. 5773579

; GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Bollon, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: SIDLEY & AUSTIN

STREET: 1201 Elm Street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,088

FILING DATE: 19-JUL-95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Eugenia S. Hansen

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 10365/05011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-981-3400

TELEFAX: 214-981-3300

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 354 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-776-088-2

Query Match 59.5%; Score 47; DB 1; Length 354;
Best Local Similarity 80.0%; Pred. No. 1.7;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PNDPSASEHT 13
1111 1111
Db 125 PNDPHGSEHT 134

RESULT 14
US-08-776-088-6
; Sequence 6, Application US/08776088
; Patent No. 5773579
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: Lung Cancer Marker
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STDLEY & AUSTIN
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,088
; FILING DATE: 19-JUL-95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Eugenia S. Hansen
; REGISTRATION NUMBER: 31,966
; REFERENCE/DOCKET NUMBER: 10365/05011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 214-981-3300
; TELEFAX: 214-981-3400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-776-088-6

Query Match 59.5%; Score 47; DB 1; Length 354;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PNDPSASEHT 13
1111 1111
Db 125 PNDPHGSEHT 134

RESULT 15
US-09-325-320-2
; Sequence 2, Application US/09325320
; Patent No. 6117981
; GENERAL INFORMATION:
; APPLICANT: Torczynski, Richard M.
; APPLICANT: Bollon, Arthur P.
; TITLE OF INVENTION: HYBRIDOMAS FOR LUNG CANCER MARKER AND MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES THEREOF
; FILE REFERENCE: 10365/06101
; CURRENT APPLICATION NUMBER: US/09/325,320
; CURRENT FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 354

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-325-320-2

Query Match 59.5%; Score 47; DB 3; Length 354;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 PNDPSASEHT 13
1111 1111
Db 125 PNDPHGSEHT 134

Search completed: February 2, 2001, 10:36:30
Job time: 43 sec

Fri Feb 2 15:15:35 2001

us-09-273-217-3.ra1

THIS PAGE IS BLANK

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 2, 2001, 10:36:30 ; Search time 34.98 Seconds
(without alignments)
7.700 Million cell updates/sec

Title: US-09-273-217-4

Sequence: 1 PEAADPTSGFSSIP 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/PCITUS_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	91.0	528	2	US-08-527-152-2
2	43	55.1	597	1	US-08-462-884A-1
3	43	55.1	597	1	US-08-461-881B-1
4	43	55.1	597	2	US-09-123-960-1
5	43	55.1	605	1	US-08-462-884A-3
6	43	55.1	605	1	US-08-461-881B-3
7	43	55.1	605	2	US-09-123-960-3
8	41	52.6	78	1	US-08-624-123-13
9	41	52.6	78	2	US-08-716-308-2
10	41	52.6	78	2	US-08-716-308-16
11	41	52.6	78	4	PCT-US96-05262-14
12	41	52.6	617	1	US-08-191-866D-58
13	41	52.6	617	2	US-08-185-949B-58
14	40	51.3	535	1	US-08-445-050-4
15	40	51.3	535	2	US-08-204-691-4
16	40	51.3	539	1	US-08-464-340A-13
17	40	51.3	546	1	US-08-445-050-5
18	40	51.3	546	2	US-08-204-691-5
19	40	51.3	568	1	US-08-445-050-6
20	40	51.3	568	2	US-08-204-691-6
21	40	51.3	521	5	5200183-17
22	40	51.3	668	1	US-08-445-050-9
23	40	51.3	668	2	US-08-204-691-9
24	40	51.3	722	1	US-08-347-718B-1
25	40	51.3	722	1	US-08-445-050-3
26	40	51.3	722	1	US-08-445-050-7
27	40	51.3	722	2	US-08-482-262-1
28	40	51.3	722	2	US-08-204-691-3

29	40	51.3	722	2	US-08-204-691-7	Sequence 7, Appli
30	40	51.3	722	5	5200183-3	Patent No. 5200183
31	40	51.3	742	1	US-08-347-718B-2	Sequence 2, Appli
32	40	51.3	742	2	US-08-482-262-2	Sequence 2, Appli
33	40	51.3	742	5	5200183-2	Patent No. 5200183
34	40	51.3	745	1	US-08-445-050-2	Sequence 2, Appli
35	40	51.3	745	2	US-08-204-691-2	Sequence 2, Appli
36	40	51.3	745	3	US-08-370-223-13	Sequence 13, Appli
37	39	50.0	51	1	US-07-689-693B-21	Sequence 21, Appli
38	39	50.0	78	1	US-07-689-693B-5	Sequence 5, Appli
39	39	50.0	723	5	5200183-4	Patent No. 5200183
40	37	47.4	532	1	US-08-288-405A-10	Sequence 10, Appli
41	37	47.4	615	2	US-08-738-349-12	Sequence 12, Appli
42	37	47.4	693	2	US-08-738-349-6	Sequence 6, Appli
43	37	47.4	796	1	US-08-188-228-58	Sequence 58, Appli
44	37	47.4	796	1	US-08-332-643-52	Sequence 52, Appli
45	37	47.4	796	1	US-08-332-638-58	Sequence 58, Appli

ALIGNMENTS

RESULT 1
US-08-527-152-2
Sequence 2, Application US/08527152
Patent No. 5827655
GENERAL INFORMATION:
APPLICANT: Chandu, Kantanthara G.
APPLICANT: Cahalan, Michael D.
APPLICANT: Grissmer, Stephan
APPLICANT: Goldin, Alan L.
APPLICANT: Guthrie, Brent A.
APPLICANT: Gutman, George A.
APPLICANT: Masumth, John J.
TITLE OF INVENTION: Assay, Methods and Products Based On n
TITLE OF INVENTION: K+ Channel Expression
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/527,152
FILING DATE: UNKNOWN
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/170,418
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,568
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-54444-2/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-527-152-2

Query Match 91.0%; Score 71; DB 2; Length 528;
Best Local Similarity 86.7%; Pred. No. 3,2e-05;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAEADDPGSGSSIP 15
Db 371 FAEADDPGSGSSIP 385

RESULT 2
US-08-462-884A-1
; Sequence 1, Application US/08462884A
; Patent No. 5624836
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic Cholesterol
; TITLE OF INVENTION: Esterase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Banner & Allegretti
; STREET: 10 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,884A
; FILING DATE: Unknown
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/715-1000
; TELEFAX: 312/715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..597
; OTHER INFORMATION: /note="Bovine pancreatic
; OTHER INFORMATION: cholesterol esterase"
US-08-462-884A-1

Query Match 55.1%; Score 43; DB 1; Length 597;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAEADDPGSGSSIP 15
Db 489 FARTGDPWGHSTVP 503

RESULT 3
US-08-461-881B-1
; Sequence 1, Application US/08461881B

; Patent No. 5792832
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic Cholesterol Esterase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,881B
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Blair Hughes
; REGISTRATION NUMBER: 32,901
; REFERENCE/DOCKET NUMBER: 89,852-J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/913-0001
; TELEFAX: 312/913-0002
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..597
; OTHER INFORMATION: /note="Bovine pancreatic
; OTHER INFORMATION: cholesterol esterase"
US-08-461-881B-1

Query Match 55.1%; Score 43; DB 1; Length 597;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAEADDPGSGSSIP 15
Db 489 FARTGDPWGHSTVP 503

RESULT 4
US-09-123-960-1
; Sequence 1, Application US/09123960
; Patent No. 5981299
; GENERAL INFORMATION:
; APPLICANT: Lange III, Louis G
; APPLICANT: Spilburg, Curtis A
; TITLE OF INVENTION: Mammalian Pancreatic
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" hard disc
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS


```

GENERAL INFORMATION:
APPLICANT: Lange III, Louis G
APPLICANT: Spilburg, Curtis A
TITLE OF INVENTION: Mammalian Pancreatic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" hard disc
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,960
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,881
FILING DATE: June 5, 1995
ATTORNEY/AGENT INFORMATION:
NAME: A. Blair Hughes
REGISTRATION NUMBER: 32,901
REFERENCE/DOCKET NUMBER: 89,852-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/913-0001
TELEFAX: 312/913-0002
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-960-3

Query Match          55.1%; Score 43; DB 2; Length 605;
Best Local Similarity 46.7%; Pred. No. 5.4;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 FAADDPGSGSSIP 15
Db 497 FARTGDPNGHSTYP 511

RESULT 8
US-08-624-123-13
Sequence 13, Application US/08624123
Patent No. 5739276
GENERAL INFORMATION:
APPLICANT: Shon, Ki-Joon
APPLICANT: Grille, Michelle M.
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/624,123
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,554
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/423,561
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107674-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-624-123-13

Query Match          52.6%; Score 41; DB 1; Length 78;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 FAADDPGSGSSIP 14
Db 19 FARTDPPRNGHNT 32

RESULT 9
US-08-716-308-2
Sequence 2, Application US/08716308
Patent No. 5885569
GENERAL INFORMATION:
APPLICANT: Windass, John D.
TITLE OF INVENTION: Biological Insect Control Agent
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENeca Inc.
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,308
FILING DATE: 24-SEP-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00677
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9405951.6
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschultz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD40027X/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 2:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-308-2

```

Query Match	52.6%;	Score 41;	DB 2;	Length 78;
Best Local Similarity	50.0%;	Pred. No. 1.1;		
Matches	7;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;

```
QY      1  FAEADPTSGFSSI 14
        ||||| : | ::
Db     19  FATADDPRLGNTL 32
```

RESULT 10
US-08-716-308-16
; Sequence 16, Application US/08716308

? GENERAL INFORMATION:
 ? APPLICANT: Windass, John D.
 ? TITLE OF INVENTION: Biological Insect Control Agent
 ? NUMBER OF SEQUENCES: 18
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: ZENECA INC.
 ? STREET: 1800 Concord Pike
 ? CITY: Wilmington
 ? STATE: DE
 ? COUNTRY: USA
 ? ZIP: 19850
 ?

```

: COMPUTER READABLE FORM.:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/716,308
: FILING DATE: 24-SEP-1996
: CLASSIFICATION: 42A
: PRIOR APPLICATION DATA:

```

Query Match	52.6%	Score 41	DB 2	Length 78
Best Local Similarity	50.0%	Pred. No. 1.1		
Best Local Similarity	50.0%	Pred. No. 1.1		
Matches 7; Conservative		3; Mismatches	4; Indels	0; Gaps

```
QY      1 FAEADDP TSG FSSI 14
        || |||| : || :
Db      19 FATADDP R NGLG NL 32
```

RESULT 11
PCT-US96-05262-14

```
; Sequence 14, Application PC/TUS9605262
; GENERAL INFORMATION:
```

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

COMPUTER READABLE FORM:

1 MEDIUM TYPE: Floppy disk
 2 COMPUTER: IBM PC compatible
 3 OPERATING SYSTEM: PC-DOS/MS-DOS
 4 SOFTWARE: Patentin Release #1.0, Version #1.30
 5 CURRENT APPLICATION DATA:
 6 APPLICATION NUMBER: PCT/US96/05262
 7 FILING DATE: 17-APR-1996

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/423,561

```

1 FILING DATE: 17-APR-1995
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Saxe, Stephen A.
4 REGISTRATION NUMBER: 38,609
5 REFERENCE/DOCKET NUMBER: 24260-107674
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 202-962-4848

? TELEFAX: 202-962-8300
 ? INFORMATION FOR SEQ. ID NO:
 ? SEQUENCE CHARACTERISTICS
 ? LENGTH: 78 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? :
 ? HYPOTHETICAL: NO
 ? :
 PCT-US96-05262-14

Query Match	52.68;	Score 41;	DB 4;	Length 78;
Best Local Similarity	50.08;	Pred. No. 1.1;		
Matches	7;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0

```
QY      1 FAEADPTSGFSSI 14
        |||||:|::
Db     19 FATADDPRLNGNL 32
```

```

;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
US-08-716-308-16
.

RESULT 12
US-08-191-866D-58
; Sequence 58, Application US/08191866C

```

```

Query Match      5.6%; Score 41; DB 2; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      1 FAADDPGSGSSI 14
        ||||| : : :

```

STATE: New York
COUNTRY: USA

Query Match	51.3%	Score 40;	DB 1;	Length 535;
Best Local Similarity	46.7%;	Pred. NO. 17;		
Matches	7;	Conservative	3;	Mismatches 5; Indels 0; Gaps 0;

```
QY      1 FAEADDP TSG FSSIP 15
         ||: || | |:|
Db      471 FAKTGDP NMGDSAVP 485
```

RESULT 15

```

US-08-204-691-4
: Sequence 4, Application US/08204691
: Patent No. 5827683
:
: GENERAL INFORMATION:
:
: APPLICANT: Blackberg, Lars
: APPLICANT: Edlund, Michael
: APPLICANT: Hansson, Lennart
: APPLICANT: Herneli, Olle
: APPLICANT: Lundberg, Lennart
: APPLICANT: Stromqvist, Mats
:
: APPLICANT: Toernell, Jan
:
: TITLE OF INVENTION: No. 5827683el Polypeptides
:
: NUMBER OF SEQUENCES: 21
:
: CORRESPONDENCE ADDRESSES:
:
: ADDRESSEE: White & Case
:
: STREET: 1155 Avenue of the Americas
:
: CITY: New York
:
: STATE: New York
:
: COUNTRY: United States
:
: ZIP: 10036-2787
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: Patentln Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/204,691
:
: FILING DATE:
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: SE 9300686-4
:
: FILING DATE: 01-MAR-1993
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: SE 9300722-7
:
: FILING DATE: 04-MAR-1993
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Sterner Ph.D., Richard J
:
: REGISTRATION NUMBER: 35,372
:
: REFERENCE/DOCKET NUMBER: 1103262-850
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (212)819-8783
:
: TELEFAX: (212)354-8113
:
: INFORMATION FOR SEQ ID NO: 4:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 535 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: HYPOTHEICAL: NO
:
: ORIGINAL SOURCE:
:
: ORGANISM: Homo sapiens
:
: TISSUE TYPE: Mammary gland
:
: FEATURE:
:
: NAME/KEY: Peptide
:
: LOCATION: 1..535
:
: OTHER INFORMATION: /label= Variant_A
:
US-08-204-691-4

```

```
QY      1 FAEADPTSGFSSIP 15
          ||: || ||:|
Db      471 FAKTGDPMGDSAVP 485
```

Search completed: February 2, 2001, 10:36:31
Job time: 44 sec

Query Match	51.38;	Score 40;	DB 2;	Length 535;
Best Local Similarity	46.78;	Pred. No. 17;		
Matches	7; Conservative	3; Mismatches	5; Indels	0; Gaps

Dist in LA
EW, incl.
